```
                    GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on:        August  4, 2005, 17:55:32 ; Search time 92.5 Seconds
                                  (without alignments)
                               677.353 Million cell updates/sec

Title:         NOLAN463-1A.SEQ
Perfect score: 140
Sequence:      1 GAAATCAATCATATGTGGAAG.........ATATTAGCAGCTCGTTAGCC 81

Scoring table: BLOSUM62
               Xgapop  10.0 , Xgapext   0.1
               Ygapop  10.0 , Ygapext   0.1
               Fgapop   6.0 , Fgapext   0.1
               Delop    6.0 , Delext    0.1

Searched:      2105592 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:        4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=x1p
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-1/runat_04082005_125805_24527/app_query.fasta_1.5
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN_1_1_308 @runat_04082005_125805_24527 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :     A_Geneseq_16Dec04:*
           1:   geneseqp1980s:*
           2:   geneseqp1990s:*
           3:   geneseqp2000s:*
           4:   geneseqp2001s:*
           5:   geneseqp2002s:*
           6:   geneseqp2002as:*
           7:   geneseqp2003bs:*
           8:   geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

                           SUMMARIES

                    %
Result         Query
No.    Score   Match  Length DB   ID          Description
----   -----   -----  ------ --   --          -----------
  1    113.1   80.8    249   5    ABP45310    Abp45310 Human BLy
  2    113.1   80.8    249   7    ADG96137    Adg96137 Single ch
  3     93.8   67.0    250   5    ABP44982    Abp44982 Human BLy
  4     93.8   67.0    250   7    ADG95809    Adg95809 Single ch
  5     93.8   67.0    253   5    ABP44943    Abp44943 Human BLy
  6     93.8   67.0    253   7    ADG95770    Adg95770 Single ch
  7     92.4   66.0     80   2    AAW62794    Aaw62794 Amino aci
  8     92.4   66.0     97   2    AAY05694    Aay05694 Multiple
  9     92.4   66.0     97   5    ABG78212    Abg78212 Human Fv
 10     92.4   66.0     97   5    ABG91903    Abg91903 Human ant
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 11   92.4   66.0   97   6   AB027107   Ab027107 Human ger
 12   92.4   66.0   97   7   ADB75646   Adb75646 Human pro
 13   92.4   66.0   97   7   ADD28104   Add28104 Lymphoma
 14   92.4   66.0   97   7   ADF10048   Adf10048 VEGF anti
 15   92.4   66.0   97   7   ADF10150   Adf10150 Antibody
 16   92.4   66.0   97   7   ADF09942   Adf09942 Antibody
 17   92.4   66.0   97   7   ADJ80323   Adj80323 VH gene 1
 18   92.4   66.0  114   3   AAB01949   Aab01949 Anti-Id1
 19   92.4   66.0  114   3   AAB01950   Aab01950 Anti-Id1
 20   92.4   66.0  114   3   AAB01953   Aab01953 Anti-Id1
 21   92.4   66.0  114   3   AAB01959   Aab01959 High affi
 22   92.4   66.0  114   3   AAB01952   Aab01952 Anti-Id1
 23   92.4   66.0  114   3   AAB01955   Aab01955 Strepativ
 24   92.4   66.0  114   3   AAB01956   Aab01956 Strepativ
 25   92.4   66.0  114   3   AAB01948   Aab01948 Wild-type
 26   92.4   66.0  114   7   ADG70086   Adg70086 Diversifi
 27   92.4   66.0  114   7   ADG70013   Adg70013 Diversifi
 28   92.4   66.0  116   2   AAR66324   Aar66324 Human imm
 29   92.4   66.0  117   4   AAM60904   Aam60904 Human bra
 30   92.4   66.0  117   4   ABG55317   Abg55317 Human liv
 31   92.4   66.0  117   5   ABG43454   Abg43454 Human pep
 32   92.4   66.0  118   6   ADA89246   Ada89246 Human ant
 33   92.4   66.0  122   6   ADK17418   Adk17418 Anti-huma
 34   92.4   66.0  122   8   ADG42840   Adg42840 scFv Abl2
 35   92.4   66.0  123   2   AAW03757   Aaw03757 Anti-rhes
 36   92.4   66.0  125   6   ADA89266   Ada89266 Human ant
 37   92.4   66.0  125   6   ADA89274   Ada89274 Human ant
 38   92.4   66.0  139   3   AAY99556   Aay99556 Human LH1
 39   92.4   66.0  139   6   ABR42859   Abr42859 Tumour-sp
 40   92.4   66.0  139   7   ABW02445   Abw02445 Human mon
 41   92.4   66.0  142   6   ABP96287   Abp96287 Anti-hTNF
 42   92.4   66.0  154   6   ABP96293   Abp96293 Human ant
 43   92.4   66.0  190   2   AAY33304   Aay33304 IgM antib
 44   92.4   66.0  202   2   AAY34303   Aay34303 IgM antib
 45   92.4   66.0  205   2   AAY34299   Aay34299 IgM antib
```

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                                   ALIGNMENTS

RESULT 1
ABP45310
ID   ABP45310 standard; protein; 249 AA.
XX
AC   ABP45310;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1321.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cycostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO20020202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
```

PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1979-1980; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

Alignment Scores:
Pred. No.:   2.44e-05   Length: 249
Score: 113.10   Matches: 26
Percent Similarity: 20.63%   Conservative: 1
Best Local Similarity: 20.63%   Mismatches: 0
Query Match: 80.79%   Indels: 99
DB: 5   Gaps: 1

NOLAN463-1A.SEQ (1-81) x ABP45310 (1-249)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGT----------- 48
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 --- 48

Db   70 SerValAspThrSerLysAspGlnPheSerLeuLysSerSerValThrAlaAlaAsp 89

Qy   48 --- 48

Db   90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrTyrArg 109

Qy   48 --- 48

Db   110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129

Qy   48 --- 48

Db   130 GlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGlnSerPro 149

Qy   49 ---------------------------------------CGGGCGAGTCAGGAT 63
                                                  ||||||||||||||
Db   150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169

Qy   64 ATTAGCAGCTGGTTAGCC 81
          |||||||||||||||||||
Db   170 IleSerSerTrpLeuAla 175

RESULT 2
ADG96137
ID   ADG96137 standard; protein; 249 AA.
XX
AC   ADG96137;
XX

DT   11-MAR-2004 (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 1321.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO200305979-A2.
XX
PD   10-JUL-2003.
XX
PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 1321; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 249 AA;

Alignment Scores:
Pred. No.:   2.44e-05   Length: 249
Score: 113.10   Matches: 26
Percent Similarity: 20.63%   Conservative: 0
Best Local Similarity: 20.63%   Mismatches: 1
Query Match: 80.79%   Indels: 99
DB: 7   Gaps: 1

NOLAN463-1A.SEQ (1-81) x ADG96137 (1-249)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGT----------- 48
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 --- 48

```
Db    70  SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp  89

Qy    48  ------------------------------------------------------------  48

Db    90  ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg  109

Qy    48  ------------------------------------------------------------  48

Db   110  TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly  129

Qy    48  ------------------------------------------------------------  48

Db   130  GlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro  149

Qy    49  ---------------------------------------CGGGCGAGTCAGGAT        63
                                                  |||||||||||||||
Db   150  SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly  169

Qy    64  ATTAGCAGCTGGTTAGCC  81
          ||||||||||||||||||
Db   170  IleSerSerTrpLeuAla  175


RESULT 3
ABP44982
ID   ABP44982 standard; protein; 250 AA.
XX
AC   ABP44982;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 993.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO2002641-A1.
XX
PD   10-JAN-2002.
XX
PR   15-JUN-2001;  2001WO-US019110.
PR   16-JUN-2000;  2000US-0212210P.
PR   17-OCT-2000;  2000US-0240816P.
PR   16-MAR-2001;  2001US-0276248P.
PR   21-MAR-2001;  2001US-0277379P.
PR   25-MAY-2001;  2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1586-1587; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 250 AA;

Alignment Scores:
Pred. No.:                 0.00726        Length:              250
Score:                    93.80           Matches:              20
Percent Similarity:       80.77%          Conservative:          1
Best Local Similarity:    76.92%          Mismatches:            2
Query Match:              67.00%          Indels:                1
DB:                       5               Gaps:                  1

NOLAN463-1A.SEQ (1-81) x ABP44982 (1-250)

Qy    1  GAAATCAATCATAGTGGAAGCAACCACCACCGTCCCTCAAGAGTCGGCG-----  54
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Db   50  GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle  69

Qy   55  AGTCAGGATATTAGCAGC  72
         ||||||||||  ::::
Db   70  SerGlnAspThrSerAsn  75


RESULT 4
ADG95809
ID   ADG95809 standard; protein; 250 AA.
XX
AC   ADG95809;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 993.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2003055979-A2.
XX
PD   10-JUL-2003.
XX
PF   14-NOV-2002;  2002WO-US036496.
XX
PR   16-NOV-2001;  2001US-0331469P.
PR   19-DEC-2001;  2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 993; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
```

```
CC  necrosis factor superfamily and induces both in vivo and in vitro B cell
CC  proliferation and differentiation. Specifically, it refers to single
CC  chain antibody molecules (scFvs) derived, preferably, from the variable
CC  heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC  fragment thereof, of either human, murine, rat or monkey BLyS. The
CC  present invention refers to the use of such antibodies in various methods
CC  for the detection, diagnosis and prognosis of diseases related to the
CC  aberrant expression or inappropriate function of BLyS or its receptor. As
CC  such, these compositions are useful for identifying immune disorders
CC  including myasthenia gravis and multiple sclerosis, inflammatory
CC  disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC  as AIDS and proliferative disorders including leukaemia, carcinoma and
CC  lymphoma. Accordingly, they can be described as exhibiting various
CC  activities such as antirheumatic, antiarthritic, neuroprotective,
CC  antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC  polypeptide sequence is a single chain antibody that binds BLyS of the
CC  invention. NOTE: The sequence data for this patent did not form part of
CC  the printed specification, but was obtained in electronic format
CC  directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ  Sequence 250 AA;

Alignment Scores:
Pred. No.:              0.00726        Length:           250
Score:                  93.80          Matches:          20
Percent Similarity:     80.77%         Conservative:     1
Best Local Similarity: 76.92%         Mismatches:       3
Query Match:            67.00%         Indels:           2
DB:                                    Gaps:             1

NOLAN463-1A.SEQ (1-81) x ADG95809 (1-250)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGTCGGGCG------ 54
         |||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy  55 AGTCAGGATATTAGCAGC 72
         |||||||||| |||:::
Db  70 SerGlnAspThrSerAsn 75

RESULT 5
ABP44943
ID  ABP44943 standard; protein; 253 AA.
XX
AC  ABP44943;
XX
DT  19-AUG-2002  (first entry)
XX
DE  Human BLyS binding scFv SEQ ID 954.
XX
KW  BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW  tumour necrosis factor; B cell proliferation; B cell differentiation;
KW  immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW  antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW  systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW  common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS  Homo sapiens.
XX
PN  WO200202641-A1.
XX
PD  10-JAN-2002.
XX
PF  15-JUN-2001; 2001WO-US019110.
XX
PR  16-JUN-2000; 2000US-0212210P.
PR  17-OCT-2000; 2000US-0240816P.
PR  16-MAR-2001; 2001US-0276248P.
PR  21-MAR-2001; 2001US-0277379P.
PR  25-MAY-2001; 2001US-0293499P.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
PA  (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
```

```
XX
PI  Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR  WPI; 2002-114799/15.
XX
PT  Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT  diagnosis and treatment of cancers and immune disorders.
XX
PS  Claim 1; Page 1540-1541; 3148pp; English.
XX
CC  This invention describes novel antibodies that immunospecifically bind to
CC  B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC  tumour necrosis factor (TNF) super family and induces B cell
CC  proliferation and differentiation. The antibodies of the invention have
CC  cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC  antirheumatic and antiAIDS activity and can be used in vaccines to
CC  inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC  and so may be used to detect and quantitate the presence of BLyS in
CC  biological samples and may be used in this way to diagnose disease
CC  associated with aberrant expression of BLyS. They may also be
CC  administered to treat diseases associated with aberrant BLyS expression
CC  and activity such as cancer, immune, and autoimmune disorders and
CC  diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC  immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC  acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC  the antibodies and fragments of the antibodies described in the method of
CC  the invention
XX
SQ  Sequence 253 AA;

Alignment Scores:
Pred. No.:              0.00728        Length:           253
Score:                  93.80          Matches:          20
Percent Similarity:     80.77%         Conservative:     1
Best Local Similarity: 76.92%         Mismatches:       3
Query Match:            67.00%         Indels:           2
DB:                                    Gaps:             1

NOLAN463-1A.SEQ (1-81) x ABP44943 (1-253)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGTCGGGCG------ 54
         |||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy  55 AGTCAGGATATTAGCAGC 72
         |||||||||| |||:::
Db  70 SerGlnAspThrSerAsn 75

RESULT 6
ADG95770
ID  ADG95770 standard; protein; 253 AA.
XX
AC  ADG95770;
XX
DT  11-MAR-2004  (first entry)
XX
DE  Single chain antibody that immunospecifically binds BLyS SeqID 954.
XX
KW  antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW  B cell proliferation; differentiation; scFv; myasthenia gravis;
KW  multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW  carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW  antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS  Unidentified.
XX
PN  WO200305979-A2.
XX
AC  ADG95770;
XX
PD  10-JUL-2003.
XX
PF  14-NOV-2002; 2002WO-US036496.
XX
PR  16-NOV-2001; 2001US-0331469P.
```

PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 954; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ   Sequence 253 AA;

Alignment Scores:
Pred. No.:   0.00728   Length: 253
Score: 93.80   Matches: 20
Percent Similarity: 80.77%   Conservative: 1
Best Local Similarity: 76.92%   Mismatches: 3
Query Match: 67.00%   Indels: 2
DB: 7   Gaps: 1

NOLAN463-1A.SEQ (1-81) x ADG95770 (1-253)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCG------ 54
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
         ||||||||| ||| :::
Db   70 SerGlnAspThrSerAsn 75

RESULT 7
AAW62794
ID   AAW62794 standard; peptide; 80 AA.
XX
AC   AAW62794;
XX
DT   23-SEP-1998 (first entry)
XX
DE   Amino acid sequence of a human antibody fragment.
XX
KW   Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW   inactivated endogenous Ig locus; B-cell development;
KW   human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW   kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW   production; antibody.
XX

OS   Homo sapiens.
XX
PN   WO924891-A2.
XX
PD   11-JUN-1998.
XX
PF   03-DEC-1997; 97WO-US023091.
XX
PR   03-DEC-1996; 96US-00759620.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX
DR   WPI; 1998-333314/29.
XX
PT   New transgenic non-human mammals - having an inactivated immunoglobulin
PT   locus and a near complete human immunoglobulin locus, used for production
PT   of human antibodies.
XX
PS   Disclosure; Page 71; 128pp; English.
XX
CC   AAW62793-822 represent fragments of human antibodies produced by
CC   transgenic Xenomice, created using the method of the invention. The
CC   specification describes a transgenic non-human mammal which has genome
CC   modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC   locus, so that the mammal does not display normal B-cell development. The
CC   modified genome also has an inserted human heavy chain Ig locus in
CC   germline configuration, the human heavy chain Ig locus comprising a human
CC   micro constant region and regulatory and switch sequences, human J-H
CC   genes, human D-H genes, and human V-H genes and an inserted human kappa
CC   light chain Ig locus in germline configuration, the human kappa light
CC   chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC   and V-kappa genes, where the number of V-H and V-kappa genes inserted are
CC   selected to restore normal B-cell development in the mammal. The
CC   transgenic animals have a near complete human Ig locus, including both a
CC   human heavy chain locus and a human kappa light chain locus. They can be
CC   used for the production of human antibodies when exposed to particular
CC   antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC   will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
SQ   Sequence 80 AA;

Alignment Scores:
Pred. No.:   0.00804   Length: 80
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 2   Gaps: 0

NOLAN463-1A.SEQ (1-81) x AAW62794 (1-80)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGGAGTCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   33 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 51

Qy   61 GATATTAGC 69
         |||||
Db   52 ---IleSer 53

RESULT 8
AAY05694
ID   AAY05694 standard; protein; 97 AA.
XX
AC   AAY05694;
XX
DT   19-JUL-1999 (first entry)
XX
DE   Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
XX
KW   Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
KW   heavy chain variable region; VH gene; somatic hypermutation;
XX

KW   B-cell clonality; RA gene; diagnosis; human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   1..30
FT   /label= FR1
FT   Misc-difference 8
FT   /note= "encoded by GGC"
FT   Misc-difference 13
FT   /note= "replaces Glu of RA"
FT   Misc-difference 14
FT   /note= "encoded by CCT"
FT   Misc-difference 23
FT   /note= "replaces Gly of RA"
FT   Misc-difference 25
FT   /note= "replaces Phe of RA"
FT   Misc-difference 30
FT   /note= "replaces Gly of RA"
FT   Region   31..36
FT   /label= CDR1
FT   Misc-difference 31
FT   /note= "replaces Gly of RA"
FT   Misc-difference 32
FT   /note= "replaces Phe of RA"
FT   Region   37..50
FT   /label= FR2
FT   Region   51..66
FT   /label= CDR2
FT   Misc-difference 56
FT   /note= "replaces Asn of RA"
FT   Misc-difference 57
FT   /note= "replaces Ser of RA"
FT   Misc-difference 58
FT   /note= "replaces Lys of RA"
FT   Region   67..97
FT   /label= FR3
FT   Misc-difference 71
FT   /note= "replaces Leu of RA"
FT   Misc-difference 81
FT   /note= "replaces Arg of RA"
XX
PN   WO9915696-A1.
XX
PD   01-APR-1999.
XX
PF   17-SEP-1998; 98WO-CA000873.
XX
PR   19-SEP-1997; 97CA-02216595.
PR   04-NOV-1997; 97CA-02220245.
XX
PA   (QINY/) QIN Y.
XX
PI   Qin Y;
XX
DR   WPI; 1999-276985/23.
DR   N-PSDB; AAX25318.
XX
PT   Determination of B-cell clonality by amplification or enzymatic
PT   digestion.
XX
PS   Disclosure; Fig 9D; 67pp; English.
XX
CC   This sequence represents a heavy chain variable region (VH) as predicted
CC   from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
CC   fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
CC   B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
CC   in nucleotide and predicted amino acid (see AAY05691-94) sequences were
CC   compared with the closest known germline VH genes; for 4d76, this was RA.
CC   The results provided direct evidence that intrathecal clonally expanded B
CC   -cells from the CSF of MS patients are hypermutated postgerminal centre
CC   antibody-forming or memory lymphocytes that havd undergone antigen
CC   selection. This finding implicates an important pathogenic pathway for

CC   the development of demyelination in CNS of MS. The invention provides
CC   assay kits for determining B-cell or T-cell clonality. This technology
CC   allows the establishment of clonal specific RNA library from pathogenic
CC   cells in the CNS of patients, which is important for further
CC   understanding of the role of antigen(s) in the cause of B-cell clonal
CC   expansion, and towards developing antigen specific therapeutic strategy
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00847   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 2   Gaps: 0

NOLAN463-1A.SEQ (1-81) x AAY05694 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGACCACCAACTACACCCGTCCCTCAAGAGTCGGGCGGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 9
ABG78212
ID   ABG78212 standard; protein; 97 AA.
XX
AC   ABG78212;
XX
DT   15-NOV-2002 (first entry)
XX
DE   Human Fv molecule hypervariable region related peptide #87.
XX
KW   Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW   disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW   lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200259264-A2.
XX
PD   01-AUG-2002.
XX
PF   31-DEC-2001; 2001WO-US049440.
XX
PR   29-DEC-2000; 2000US-0075181.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI   Plaksin D, Peretz T;
XX
DR   WPI; 2002-619166/66.
XX
PT   Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT   or fragment, or construct of fragment with enhanced binding
PT   characteristics so as to selectively bind target cell in favor of other
PT   cells.
XX
PS   Claim 13; Page 193; 232pp; English.
XX
CC   The invention relates to a peptide or polypeptide comprising an Fv
CC   molecule, a construct or fragments or a construct of a fragment with
CC   enhanced binding characteristics which selectively and/or specifically
CC   binds to a target cell in favour of other cells, where binding is
CC   primarily determined by a first hypervariable region and Fv is a single
CC   chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC   association with or attached, coupled, combined, linked or fused to a
CC   pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00847   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: Gaps: 0

NOLAN463-1A.SEQ (1-81) x ABG78212 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db 50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69
        ||||||
Db 69 ---IleSer 70

RESULT 10
ABG91903
ID ABG91903 standard; protein; 97 AA.
XX
AC ABG91903;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #87.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 269; 0pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one

---

CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX
SQ Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00847   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: Gaps: 0

NOLAN463-1A.SEQ (1-81) x ABG91903 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db 50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69
        ||||||
Db 69 ---IleSer 70

RESULT 11
ABG27107
ID ABG27107 standard; protein; 97 AA.
XX
AC ABG27107;
XX
DT 10-SEP-2003 (first entry)
XX
DE Human germline heavy chain variable region gene segment #40.
XX
KW Human; heavy chain variable region; VH; humanised antibody;
KW chimeric antibody; complementarity determining region; CDR;
KW canonical CDR structure type.
XX
OS Homo sapiens.
XX
PN US2003039649-A1.
XX
PD 27-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194975.
XX
PR 12-JUL-2001; 2001US-0305111P.
XX
PA (FOOT/) FOOTE J.
XX
PI Foote J;
XX
DR WPI; 2003-492151/46.
XX
PT Making humanized antibody for converting antibody, by making chimeric
PT antibodies containing complementarity determining region from non-human
PT antibody and appropriate framework sequences of human antibodies.
XX
PS Example 1; Fig 1; 31pp; English.

XX
CC   The invention describes a method of making a humanised antibody,
CC   comprising making chimeric antibodies containing a complementarity
CC   determining region (CDR) from a non-human antibody and appropriate
CC   framework sequences (I) of human antibodies. (I) is selected by using
CC   canonical CDR structure types of non-human antibody in comparison to
CC   germline canonical CDR structure types of human antibodies as the basis
CC   for selection, for humanisation. The method is useful for making a
CC   humanised antibody or a converted antibody. The method is applicable for
CC   converting a subject antibody sequence of any subject species to a less
CC   immunogenic form suitable for use in an object species. The method is
CC   reliable for identifying suitable human framework sequences to support
CC   non-human CDR regions and to provide humanised antibodies that retain
CC   high antigen binding with low immunogenicity in humans, without the need
CC   for direct comparison of framework sequences, without the need for
CC   determining critically important amino acid residues in the framework,
CC   and without the need for multiple iteration and construction to obtain
CC   humanised antibodies with suitable therapeutic properties. The antibody
CC   has high affinity and low immunogenicity without need for comparing
CC   framework sequences between non-human and human antibodies. This sequence
CC   represents a human heavy chain variable region gene segment used in the
CC   creation of humanised antibodies
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00847   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 7   Gaps: 0

NOLAN463-1A.SEQ (1-81) x ABO27107 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
         ||||||
Db   69 ---IleSer 70

RESULT 12
ADB75646
ID   ADB75646 standard; protein; 97 AA.
XX
AC   ADB75646;
XX
DT   04-DEC-2003   (first entry)
XX
DE   Human protein relating to the invention SEQ ID NO:55.
XX
KW   antibody library; CD1 region; CD2 region; VH region; VL region;
KW   immunoglobulin; CD3 region; TM1 scFv; human.
XX
OS   Homo sapiens.
XX
PN   WO200304198-A1.
XX
PD   30-MAY-2003.
XX
PF   22-NOV-2002; 2002WO-JP012236.
XX
PR   22-NOV-2001; 2001JP-00358602.
XX
PA   (UYKE-) UNIV KEIO.
XX
PI   Shimizu N,   Takayanagi A,   Okui M;
XX
DR   WPI; 2003-449818/42.
XX
PT   Highly stable artificial antibody libraries with super-repertory and

PT   little contamination from unexpressible ones, useful as tool in
PT   proteomics and e.g. for diagnosis and treating various diseases.
XX
PS   Disclosure; Page 101; 108pp; Japanese.
XX
CC   The invention relates to a novel artificial single-stranded antibody
CC   library with superior-repertory. The library is created by using a cDNA
CC   library as template for amplifying a fragment containing the CD1 and CD2
CC   regions of the VH or VL region of immunoglobulin gene and a fragment
CC   containing the CD3 region by PCR, respectively, producing VH and VL
CC   libraries, transferring into a host, and displaying the single-stranded
CC   antibody on a phage surface. An antibody library of the invention is
CC   useful as a tool in proteomics and antibody chips and filters, for
CC   screening ligands for antigens, and for studying protein-DNA interaction,
CC   diagnosis and treating various diseases. The present sequence represents
CC   a protein of the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00847   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 7   Gaps: 0

NOLAN463-1A.SEQ (1-81) x ADB75646 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
         ||||||
Db   69 ---IleSer 70

RESULT 13
ADD28104
ID   ADD28104 standard; protein; 97 AA.
XX
AC   ADD28104;
XX
DT   15-JAN-2004   (first entry)
XX
DE   Lymphoma related immunoglobulin variable region F5.
XX
KW   B-cell; malignant; immunoglobulin; immunoglobulin variable region;
KW   Ig variable region; glycosylation site; lymphoma; B cell receptor;
KW   cytostatic; gene therapy; glycosylation inhibitor;
KW   non-Hodgkin's lymphoma.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003074059-A2.
XX
PD   12-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-GB000783.
XX
PR   07-MAR-2002; 2002GB-00005395.
XX
PA   (CANC-) CANCER RES TECHNOLOGY LTD.
XX
PI   Zhu D,   Stevenson F;
XX
DR   WPI; 2003-902720/82.
XX
PT   Classifying a B-cell as malignant or normal by isolating a sequence
PT   representing an Ig variable region from the B cell, detecting the
PT   presence of a glycosylation site and classifying the cell as malignant or
PT   normal.

```
XX
PS  Disclosure; Fig 4; 61pp; English.
XX
CC  The present invention describes a method for classifying a B-cell as
CC  malignant or normal comprising: (a) isolating a sequence representing an
CC  immunoglobulin (Ig) variable region from the B cell; (b) detecting the
CC  presence of a glycosylation site; and (c) classifying the cell as
CC  malignant or normal on the basis of the presence or absence of a
CC  glycosylation site. Also described: (1) treating a patient suffering from
CC  or at risk of having lymphoma; (2) screening for substances capable of
CC  inhibiting glycosylation of the Ig variable region of the B cell receptor
CC  ; and (3) screening for substances (S) capable of inhibiting the
CC  interaction between lectins of the type found in the germinal centre and
CC  N-glycans found on the surface of Ig of lymphoma cells. (S) has
CC  cytostatic activity, and can be used in gene therapy, and as a
CC  glycosylation inhibitor. The method is useful in classifying a B-cell as
CC  malignant or normal. The glycosylation inhibitor is useful in preparing a
CC  medicament for treating non-Hodgkin's lymphoma. The present sequence
CC  represents an Ig variable region sequence which is used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.00847      Length:            97
Score:                  92.40        Matches:           19
Percent Similarity:     74.07%       Conservative:      1
Best Local Similarity:  70.37%       Mismatches:        1
Query Match:            66.00%       Indels:            6
DB:                                  Gaps:              0

NOLAN463-1A.SEQ (1-81) x ADD28104 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||     |||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        |||||
Db   69 ---IleSer 70

RESULT 14
ADF10048
ID  ADF10048 standard; protein; 97 AA.
XX
AC  ADF10048;
XX
DT  12-FEB-2004 (first entry)
XX
DE  VEGF antibody heavy chain variable region VH_4-34.
XX
KW  Antibody; stability; solubility; antigen binding affinity;
KW  variable region; human; VEGF.
XX
OS  Homo sapiens.
XX
PN  WO2003074679-A2.
XX
PD  12-SEP-2003.
XX
PF  03-MAR-2003; 2003WO-US006598.
XX
PR  01-MAR-2002; 2002US-0360843P.
PR  29-MAY-2002; 2002US-0384197P.
XX
PA  (XENC-) XENCOR.
XX
PI  Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR  WPI; 2003-722066/68.
XX
PT  Computer optimization of physicochemical properties of antibodies
PT  comprises analyzing the interactions of amino acids at variable
```

```
PT  positions.
XX
PS  Example 6; Fig 16a; 135pp; English.
XX
CC  The present invention relates to a method for optimizing at least one
CC  physico-chemical property of an antibody by a computational screening
CC  method. The method comprises: receiving a template antibody structure;
CC  selecting at least one variable position belonging to the antibody
CC  structure; selecting at least one amino acid to be considered at the
CC  variable position(s); analyzing the interaction of each selected amino
CC  acid at each variable position with at least part of the remainder of the
CC  antibody, including the selected amino acids at other variable positions;
CC  and identifying a set of at least one antibody sequence with at least one
CC  optimized physico-chemical property. The method is useful for optimizing
CC  the physico-chemical properties of an antibody, especially the stability,
CC  solubility, or antigen binding affinity. The optimized antibody may be
CC  useful for treating a patient. The present sequence is an antibody
CC  variable region sequence used to illustrate the invention.
XX
SQ  Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.00847      Length:            97
Score:                  92.40        Matches:           19
Percent Similarity:     74.07%       Conservative:      1
Best Local Similarity:  70.37%       Mismatches:        1
Query Match:            66.00%       Indels:            6
DB:                                  Gaps:              0

NOLAN463-1A.SEQ (1-81) x ADF10048 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||     :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        |||||
Db   69 ---IleSer 70

RESULT 15
ADF10150
ID  ADF10150 standard; protein; 97 AA.
XX
AC  ADF10150;
XX
DT  12-FEB-2004 (first entry)
XX
DE  Antibody heavy chain variable region VH_4-34.
XX
KW  Antibody; stability; solubility; antigen binding affinity;
KW  variable region; human.
XX
OS  Homo sapiens.
XX
PN  WO2003074679-A2.
XX
PD  12-SEP-2003.
XX
PF  03-MAR-2003; 2003WO-US006598.
XX
PR  01-MAR-2002; 2002US-0360843P.
PR  29-MAY-2002; 2002US-0384197P.
XX
PA  (XENC-) XENCOR.
XX
PI  Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR  WPI; 2003-722066/68.
XX
PT  Computer optimization of physicochemical properties of antibodies
PT  comprises analyzing the interactions of amino acids at variable
PT  positions.
XX
```

PS   Example 16; Fig 40a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00847   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 7   Gaps: 0

NOLAN463-1A.SEQ (1-81) x ADF10150 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ::::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
         |||||||
Db   69 ---IleSer 70

Search completed: August 4, 2005, 18:14:24
Job time : 97.5 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August  4, 2005, 18:05:28 ; Search time 23.25 Seconds
                                (without alignments)
                                520.135 Million cell updates/sec

Title:     NOLAN463-1A.SEQ
Perfect score: 140
Sequence:  1 GAAATCAATCATAGTGGAAG.........ATATTAGCAGCTCGTTAGCC 81

Scoring table: BLOSUM62
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          Ygapop  10.0 , Ygapext   0.1
          Fgapop   6.0 , Fgapext   0.1
          Delop    6.0 , Delext    0.1

Searched:     513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:     1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
          Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN 1.1 66 @runat_04082005_125807_24557 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :   Issued Patents AA:*
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    2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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    4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
    5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
    6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.


                              SUMMARIES
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Result No.	Score	%Query Match	Length	DB	ID	Description
1	92.4	66.0	116	3	US-08-545-809A-118	Sequence 118, App
2	92.4	66.0	123	3	US-08-793-450-4	Sequence 4, Appli
3	92.4	66.0	139	4	US-09-203-768A-2	Sequence 2, Appli
4	92.4	66.0	472	3	US-08-793-450-8	Sequence 8, Appli
5	87.4	62.4	429	4	US-09-372-425A-6	Sequence 6, Appli
6	84.4	60.3	118	3	US-09-025-769B-25	Sequence 25, Appl
7	84.4	60.3	118	4	US-09-490-070A-25	Sequence 25, Appl
8	84.4	60.3	118	4	US-09-490-153-25	Sequence 25, Appl
9	84.4	60.3	118	4	US-09-490-324-25	Sequence 25, Appl
10	81	57.9	120	3	US-08-545-809A-137	Sequence 137, App
11	80.7	57.6	130	3	US-08-466-151-5	Sequence 5, Appli
12	80.7	57.6	130	3	US-08-466-163B-5	Sequence 5, Appli

13	80.7	57.6	130	4	US-09-802-096-5	Sequence 5, Appli
14	80.7	57.6	130	4	US-09-802-077-5	Sequence 5, Appli
15	79.4	56.7	147	4	US-09-471-276-835	Sequence 835, App
16	79.4	56.7	447	2	US-09-372-425A-2	Sequence 2, Appli
17	77	55.0	119	2	US-08-428-197-16	Sequence 16, Appl
18	77	55.0	119	5	PCT-US93-10555-16	Sequence 16, Appl
19	76.4	54.6	112	3	US-09-344-587-14	Sequence 14, Appl
20	75.9	54.2	118	2	US-08-652-816A-13	Sequence 13, Appl
21	74.4	53.1	120	4	US-09-424-840B-20	Sequence 20, Appl
22	73.4	52.4	21	3	US-08-918-148-45	Sequence 45, Appl
23	73.4	52.4	21	3	US-09-138-091A-45	Sequence 45, Appl
24	73.4	52.4	76	3	US-08-851-362D-22	Sequence 22, Appl
25	73.4	52.4	96	3	US-08-851-362D-35	Sequence 35, Appl
26	73.4	52.4	116	3	US-08-545-809A-140	Sequence 140, App
27	73.4	52.4	117	3	US-08-851-362D-48	Sequence 48, Appl
28	73.4	52.4	118	3	US-08-545-809A-142	Sequence 142, App
29	73.4	52.4	119	3	US-09-025-769B-39	Sequence 39, Appl
30	73.4	52.4	119	3	US-09-490-070A-39	Sequence 39, Appl
31	73.4	52.4	119	4	US-09-490-070A-39	Sequence 39, Appl
32	73.4	52.4	119	4	US-09-490-070A-65	Sequence 65, Appl
33	73.4	52.4	119	4	US-09-490-153-39	Sequence 39, Appl
34	73.4	52.4	119	4	US-09-490-153-65	Sequence 65, Appl
35	73.4	52.4	119	4	US-09-490-324-39	Sequence 39, Appl
36	73.4	52.4	119	4	US-09-490-324-65	Sequence 65, Appl
37	73.4	52.4	139	4	US-09-471-276-837	Sequence 837, App
38	73.4	52.4	244	4	US-08-918-148-79	Sequence 79, Appl
39	73.4	52.4	244	4	US-09-138-091A-77	Sequence 77, Appl
40	73	52.1	100	4	US-09-726-219A-169	Sequence 169, App
41	72.4	51.7	140	4	US-09-471-276-850	Sequence 850, App
42	72.4	51.4	240	2	US-07-956-399-2	Sequence 2, Appli
43	72	51.4	95	4	US-09-471-276-882	Sequence 882, App
44	72	51.4	116	3	US-08-545-809A-92	Sequence 92, Appl
45	72	51.4	119	3	US-08-767-128-18	Sequence 18, Appl

```
                              ALIGNMENTS

RESULT 1
US-08-545-809A-118
; Sequence 118, Application US/0854580 9A
; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT:  Honjo, Tasuku
;   APPLICANT:  Matsuda, Fumihiko
;   TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES:  145
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  Fish & Richardson, P.C.
;    STREET:  225 Franklin Street
;    CITY:  Boston
;    STATE:  MA
;    COUNTRY:  US
;    ZIP:  02110-2804
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Diskette
;    COMPUTER:  IBM Compatible
;    OPERATING SYSTEM:  Windows95
;    SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/545,809A
;    FILING DATE:  27-MAR-1996
;   PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  PCT/JP93/00603
;    FILING DATE:  10-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;    NAME:  Freeman, John W.
;    REGISTRATION NUMBER:  29,066
;    REFERENCE/DOCKET NUMBER:  06501/004001
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  617-542-5070
;    TELEFAX:  617-542-8906
;    TELEX:  200154
```

; INFORMATION FOR SEQ ID NO: 118:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 116 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-545-809A-118

Alignment Scores:
Pred. No.:   0.000752   Length: 116
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 3   Gaps: 0

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Qy   1 GAAATCAATCATATGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy   61 GATATTAGC 69
          |||||
Db   88 ---IleSer 89

RESULT 2
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
;   APPLICANT: EDELMAN, LENA
;   APPLICANT: MARGARITTE, CHRISTEL
;   APPLICANT: KACZOREK, MICHEL
;   APPLICANT: CHAABIHI, HASSAN
;   TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;   TITLE OF INVENTION:
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;   CITY: ARLINGTON
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/793,450
;   FILING DATE: 03-MAR-1997
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: FR 94/10566
;   FILING DATE: 02-SEP-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OBLON, NORMAN F.:
;   REGISTRATION NUMBER: 24,618
;   REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-413-3000
;   TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 123 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-793-450-4

Alignment Scores:
Pred. No.:   0.000768   Length: 123
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 3   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-08-793-450-4 (1-123)

Qy   1 GAAATCAATCATATGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
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Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 3
US-09-203-768A-2
; Sequence 2, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
;   APPLICANT: Huse, William D.
;   APPLICANT: Watkins, Jeffry D.
;   TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
;   TITLE OF INVENTION: of Use
;   FILE REFERENCE: P-IX 2947
;   CURRENT APPLICATION NUMBER: US/09/203,768A
;   CURRENT FILING DATE: 1998-12-02
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-203-768A-2

Alignment Scores:
Pred. No.:   0.000802   Length: 139
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 4   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-203-768A-2 (1-139)

Qy   1 GAAATCAATCATATGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
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Db   69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy   61 GATATTAGC 69
          |||||
Db   88 ---IleSer 89

RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
;   APPLICANT: EDELMAN, LENA
;   APPLICANT: MARGARITTE, CHRISTEL
;   APPLICANT: KACZOREK, MICHEL
;   APPLICANT: CHAABIHI, HASSAN
;   TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;   TITLE OF INVENTION:
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;   CITY: ARLINGTON

; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-8

Alignment Scores:
Pred. No.:   0.00124   Length: 472
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-08-793-450-8 (1-472)

Qy   1 GAAATCAATCATATGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
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Qy   61 GATATTAGC 69
        |||||
Db   88 ---IleSer 89

RESULT 5
US-09-372-425A-6
; Sequence 6, Application US/09372425A
; Patent No. 6475749
; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenakmp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 510015-223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Heavy chain without Tailpiece - AA
US-09-372-425A-6

Alignment Scores:
Pred. No.:   0.00554   Length: 429
Score: 87.40   Matches: 18
Percent Similarity: 74.07%   Conservative: 2
Best Local Similarity: 66.67%   Mismatches: 1
Query Match: 62.43%   Indels: 6
DB: Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-372-425A-6 (1-429)

Qy   1 GAAATCAATCATATGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||:::|||||||||||||||||||||||||||||||||||||||||| :::
Db   69 GluIleAspHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy   61 GATATTAGC 69
        |||||
Db   88 ---IleSer 89

RESULT 6
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:

```
              TELEPHONE:  (212)596-9000
              TELEFAX:  (212)596-9090
  INFORMATION FOR SEQ ID NO: 25:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 118 amino acids
            TYPE: amino acid
            STRANDEDNESS:
            TOPOLOGY: linear
       MOLECULE TYPE: protein
US-09-025-769B-25
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Alignment Scores:
Pred. No.:               0.00872      Length:          118
Score:                   84.40        Matches:         18
Percent Similarity:      70.37%       Conservative:    1
Best Local Similarity:   66.67%       Mismatches:      2
Query Match:             60.29%       Indels:          6
DB:                      3            Gaps:            0
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NOLAN463-1A.SEQ (1-81) x US-09-025-769B-25 (1-118)

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Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG  60
         ||| ||  |||||||||||||||||||||||||||||||||||||||||    :::
Db  50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy  61 GATATTAGC  69
         ||||||
Db  69 ---IleSer  70
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RESULT 7
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;   White & McAuliffe
;   STREET: 1666 K Street, N.W., Suite 300
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20006
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,070A
;   FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Colin G. Sandercock, Esq.
;   REGISTRATION NUMBER: 31,298
;   REFERENCE/DOCKET NUMBER: 37629-0005
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 912-2000
;   TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 118 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
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RESULT 8
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
;     APPLICANT: Knappik, Achim
;              Pack, Peter
;              Ilag, Vic
;              Ge, Liming
;              Moroney, Simon
;              Plueckthun, Andreas
;     TITLE OF INVENTION: Protein/(Poly)peptide libraries
;     NUMBER OF SEQUENCES: 373
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;        STREET: 1251 Avenue of the Americas
;        CITY: New York
;        STATE: New York
;        COUNTRY: USA
;        ZIP: 10021
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/09/490,153
;        FILING DATE: 24-Jan-2000
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: US/09/025,769B
;        FILING DATE: 18-FEB-1998
;        APPLICATION NUMBER: EP 95 11 3021.0
;        FILING DATE: 18-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;        NAME: James F. Haley, Jr., Esq.
;        REGISTRATION NUMBER: 27,794
;        REFERENCE/DOCKET NUMBER: MORPHO/5
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: (212)596-9000
;        TELEFAX: (212)596-9090
;  INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 118 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Alignment Scores:
Pred. No.:              0.00872     Length:         118
Score:                  84.40       Matches:        18
Percent Similarity:     70.37%      Conservative:   1
Best Local Similarity:  66.67%      Mismatches:     2
Query Match:            60.29%      Indels:         6
DB:                     4           Gaps:           0

NOLAN463-1A.SEQ (1-81) x US-09-490-153-25 (1-118)

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Db  50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy  61 GATATTAGC 69
          |||||
Db  69 ---IleSer 70
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RESULT 9
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10021
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,324
;   FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769
;   FILING DATE: 18-FEB-1998
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9000
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 118 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Alignment Scores:
Pred. No.:   0.00872   Length: 118
Score: 84.40   Matches: 18
Percent Similarity: 70.37%   Conservative: 1
Best Local Similarity: 66.67%   Mismatches: 2
Query Match: 60.29%   Indels: 6
DB: 4   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-490-324-25 (1-118)

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Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
         |||||  ||||||||||||||||||||||||||||||||||||||||||  :::
Db  50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy  61 GATATTAGC 69
          |||||
Db  69 ---IleSer 70
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RESULT 10
US-08-545-809A-137
; Sequence 137, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT: Honjo, Tasuku
;   APPLICANT: Matsuda, Fumihiko
;   TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES: 145
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: US
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/545,809A
;   FILING DATE: 27-MAR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP93/00603
;   FILING DATE: 10-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Freeman, John W.
;   REGISTRATION NUMBER: 29,066
;   REFERENCE/DOCKET NUMBER: 06501/004001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-542-5070
;   TELEFAX: 617-542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 137:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-545-809A-137

Alignment Scores:
Pred. No.:   0.0248   Length: 120
Score: 81.00   Matches: 15
Percent Similarity: 79.17%   Conservative: 4
Best Local Similarity: 62.50%   Mismatches: 5
Query Match: 57.86%   Indels: 0
DB: 3   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-08-545-809A-137 (1-120)

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Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
         |||||:::::||||||||||||||||||||||||||||||||||||||||||  :::
Db  69 GluIleHisSerGlySerThrTyrTyrAsnProSerLeuLysSerArgIleThrMet 88

Qy  61 GATATTAGCAGC 72
          :::  :::
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Db   89 SerValAspThr 92

RESULT 11
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Immunoglobulin Variants
;   NUMBER OF SEQUENCES: 65
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/466,151
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/466163
;   FILING DATE: 06-Jun-1995
;   APPLICATION NUMBER: 08/405617
;   FILING DATE: 15-MAR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/185899
;   FILING DATE: 26-JAN-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/879495
;   FILING DATE: 07-MAY-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/744768
;   FILING DATE: 14-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Svoboda, Craig G.
;   REGISTRATION NUMBER: 39,044
;   REFERENCE/DOCKET NUMBER: P0718P2C1D1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-1489
;   TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 130 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.:   0.028   Length: 130
Score: 80.70   Matches: 18
Percent Similarity: 47.92%   Conservative: 5
Best Local Similarity: 37.50%   Mismatches: 2
Query Match: 57.64%   Indels: 23
DB: 3   Gaps: 2

NOLAN463-1A.SEQ (1-81) x US-08-466-151-5 (1-130)

Qy   4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGT------ 57
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Db   52 IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy   58 CAGGATATTAGC--- 69
          ::|||| |||
Db   72 ArgAspThrSerLysAsnGlnPheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy   70 -----------------AGCTGGTTA 78
                          :::||||:::
Db   92 AlaThrTyrTyrCysAlaTrpVal 99

RESULT 12
US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Immunoglobulin Variants
;   FILE REFERENCE: P0718P2C1D1
;   CURRENT APPLICATION NUMBER: US/08/466,163B
;   CURRENT FILING DATE: 1995-06-06
;   PRIOR APPLICATION NUMBER: US 08/405,617
;   PRIOR FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: US 08/185,899
;   PRIOR FILING DATE: 1994-01-26
;   PRIOR APPLICATION NUMBER: US 07/879,495
;   PRIOR FILING DATE: 1992-05-07
;   PRIOR APPLICATION NUMBER: US 07/744,768
;   PRIOR FILING DATE: 1991-08-14
;   NUMBER OF SEQ ID NOS: 64
;   SEQ ID NO 5
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.:   0.028   Length: 130
Score: 80.70   Matches: 18
Percent Similarity: 47.92%   Conservative: 5
Best Local Similarity: 37.50%   Mismatches: 2
Query Match: 57.64%   Indels: 23
DB: 3   Gaps: 2

NOLAN463-1A.SEQ (1-81) x US-08-466-163B-5 (1-130)

Qy   4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGT------ 57
          |||||||||||||||:::||:::|||||||||||||||||||||||||||||| ||
Db   52 IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy   58 CAGGATATTAGC--- 69
          ::|||| |||
Db   72 ArgAspThrSerLysAsnGlnPheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy   70 -----------------AGCTGGTTA 78
                          :::||||:::
Db   92 AlaThrTyrTyrCysAlaTrpVal 99

RESULT 13
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended.
;   FILE REFERENCE: P0718P2C3US
;   CURRENT APPLICATION NUMBER: US/09/802,096
;   CURRENT FILING DATE: 2001-03-08
;   PRIOR APPLICATION NUMBER: US 08/405,617
;   PRIOR FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: US 08/185,899
;   PRIOR FILING DATE: 1994-01-26
;   PRIOR APPLICATION NUMBER: PCT/US92/06860
;   PRIOR FILING DATE: 1992-08-14
;   PRIOR APPLICATION NUMBER: US 07/879,495
;   PRIOR FILING DATE: 1992-05-07
;   PRIOR APPLICATION NUMBER: US 07/744,768
;   PRIOR FILING DATE: 1991-08-14

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;   NUMBER OF SEQ ID NOS:  64
;   SEQ ID NO 5
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-802-096-5

Alignment Scores:
Pred. No.:                0.028          Length:          130
Score:                   80.70          Matches:          18
Percent Similarity:      47.92%         Conservative:      5
Best Local Similarity:   37.50%         Mismatches:        2
Query Match:             57.64%         Indels:           23
DB:                          4          Gaps:              2

NOLAN463-1A.SEQ (1-81) x US-09-802-096-5 (1-130)

Qy     4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGCGAGT------ 57
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Db    52 IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy    58 CAGGATATTAGC------                                          69
          ::|||||   |||
Db    72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy    70 ------------AGCTGGTTA 78
                      ::|||||::
Db    92 AlaThrTyrTyrCysAlaTrpVal 99


RESULT 14
US-09-802-077-5
;   Sequence 5, Application US/09802077
;   Patent No. 6699472
;   GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
;   FILE REFERENCE: P0718P2C2US
;   CURRENT APPLICATION NUMBER: US/09/802,077
;   CURRENT FILING DATE:  2001-03-08
;   PRIOR APPLICATION NUMBER: US 08/405,617
;   PRIOR FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: US 08/185,899
;   PRIOR FILING DATE: 1994-01-26
;   PRIOR APPLICATION NUMBER: PCT/US92/06860
;   PRIOR FILING DATE: 1992-08-14
;   PRIOR APPLICATION NUMBER: US 07/879,495
;   PRIOR FILING DATE: 1992-05-07
;   PRIOR APPLICATION NUMBER: US 07/744,768
;   PRIOR FILING DATE: 1991-08-14
;   NUMBER OF SEQ ID NOS: 64
;   SEQ ID NO 5
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-802-077-5

Alignment Scores:
Pred. No.:                0.028          Length:          130
Score:                   80.70          Matches:          18
Percent Similarity:      47.92%         Conservative:      5
Best Local Similarity:   37.50%         Mismatches:        2
Query Match:             57.64%         Indels:           23
DB:                          4          Gaps:              2

NOLAN463-1A.SEQ (1-81) x US-09-802-077-5 (1-130)

Qy     4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGCGAGT------ 57
          |||||||||||||||::|||::|||||||||||||||||||||||||||   |||
Db    52 IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy    58 CAGGATATTAGC------                                          69
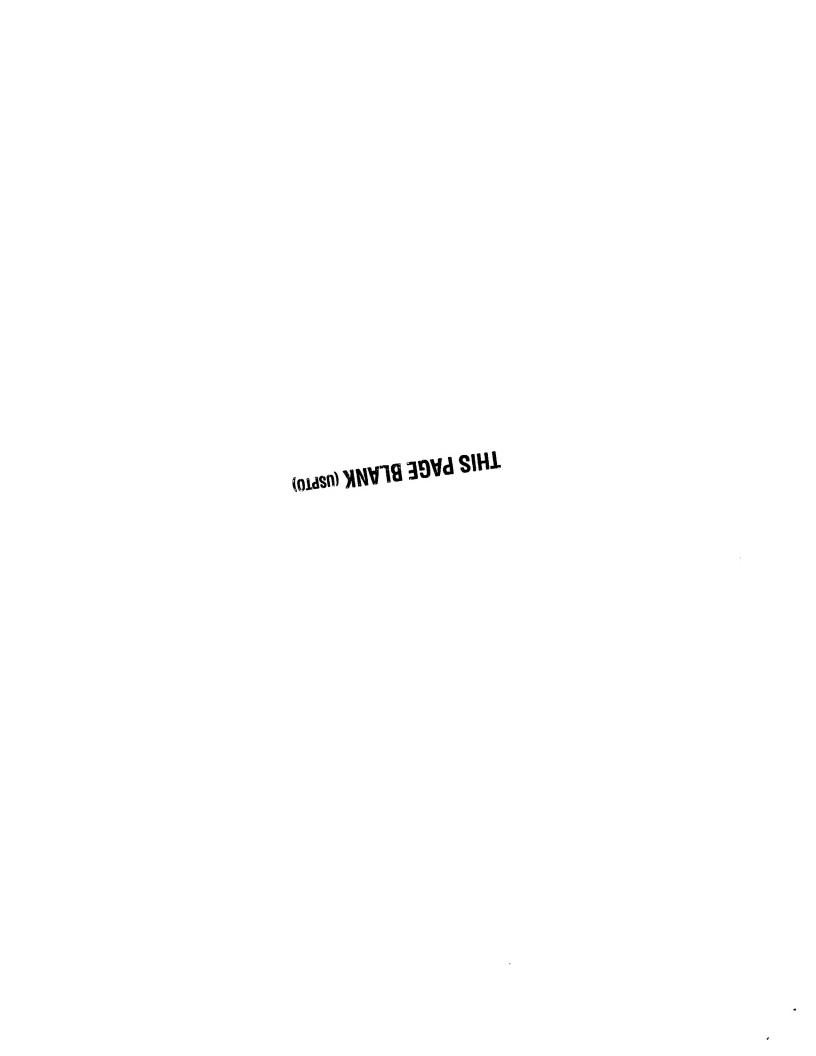          ::|||||   |||
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Db    72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy    70 ------------AGCTGGTTA 78
                      ::|||||::
Db    92 AlaThrTyrTyrCysAlaTrpVal 99


RESULT 15
US-09-471-276-835
;   Sequence 835, Application US/09471276
;   Patent No. 6822072
;   GENERAL INFORMATION:
;   APPLICANT: Dumas Milne Edwards, J.B.
;   APPLICANT: Duclert A.
;   APPLICANT: Giordano, J.Y.
;   TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;   Patent No. 6822072
;   FILE REFERENCE: GENSET.025CP1
;   CURRENT APPLICATION NUMBER: US/09/471,276
;   CURRENT FILING DATE: 1999-12-21
;   EARLIER APPLICATION NUMBER: 09/057,719
;   EARLIER FILING DATE: 1998-04-09
;   EARLIER APPLICATION NUMBER: 09/069,047
;   EARLIER FILING DATE: 1998-04-28
;   EARLIER APPLICATION NUMBER: PCT/IB99/00712
;   EARLIER FILING DATE: 1999-04-09
;   NUMBER OF SEQ ID NOS: 1622
;   SOFTWARE: Patent.pm
;   SEQ ID NO 835
;   LENGTH: 147
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -26..-1
US-09-471-276-835

Alignment Scores:
Pred. No.:                0.0435         Length:          147
Score:                   79.40          Matches:          16
Percent Similarity:      66.67%         Conservative:      2
Best Local Similarity:   59.26%         Mismatches:        3
Query Match:             56.71%         Indels:            6
DB:                          4          Gaps:              0

NOLAN463-1A.SEQ (1-81) x US-09-471-276-835 (1-147)

Qy     1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGCGAGTCAG 60
          |||::|||  |||::|||||||||||||||||||||||||||||||||||||
Db    77 GluIleAspHisGlyLyAsnThrAsnTyrAsnProSerLeuLysSerArgVal***--- 95

Qy    61 GATATTAGC 69
          |||||
Db    96 ---IleSer 97


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OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 4, 2005, 18:20:25 ; Search time 80.25 Seconds
                                       (without alignments)
                                       788.093 Million cell updates/sec

Title: NOLAN463-1A.SEQ
Perfect score: 140
Sequence: 1 GAAATCAATCATCATCTGGAAG........ATATTAGCAGCTGTTAGCC 81

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                 Fgapop 6.0 , Fgapext   0.1
                 Delop   6.0 , Delext   0.1

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 3505720

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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

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     5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
     6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
     7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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    10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
    11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
    12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
    13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
    14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
    15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
    16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
    17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
    18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
    19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
    20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
    21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
    22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	113.1	80.8	249	10	US-09-880-748-1321	Sequence 1321, Ap
2	113.1	80.8	249	15	US-10-293-418-1321	Sequence 1321, Ap
3	96.4	68.9	115	17	US-10-898-408-12	Sequence 12, Appl
4	93.8	67.0	250	10	US-09-880-748-993	Sequence 993, App
5	93.8	67.0	250	15	US-10-293-418-993	Sequence 993, App
6	93.8	67.0	253	10	US-09-880-748-954	Sequence 954, App
7	93.8	67.0	253	15	US-10-293-418-954	Sequence 954, App
8	92.4	66.0	80	14	US-10-078-958-2	Sequence 2, Appli
9	92.4	66.0	97	14	US-10-194-975-40	Sequence 40, Appl
10	92.4	66.0	97	15	US-10-308-817-83	Sequence 83, Appl
11	92.4	66.0	97	15	US-10-032-037B-87	Sequence 87, Appl
12	92.4	66.0	97	15	US-10-029-988B-87	Sequence 87, Appl
13	92.4	66.0	97	15	US-10-032-423A-87	Sequence 87, Appl
14	92.4	66.0	97	15	US-10-453-698-83	Sequence 83, Appl
15	92.4	66.0	97	15	US-10-029-926B-87	Sequence 87, Appl
16	92.4	66.0	97	16	US-10-379-392-47	Sequence 47, Appl
17	92.4	66.0	114	17	US-10-733-532-128	Sequence 128, App
18	92.4	66.0	117	9	US-09-864-761-44315	Sequence 44315, A
19	92.4	66.0	117	15	US-10-371-942-90	Sequence 90, Appl
20	92.4	66.0	118	17	US-10-893-576-192	Sequence 192, Appl
21	92.4	66.0	122	15	US-10-360-828-63	Sequence 63, Appl
22	92.4	66.0	125	15	US-10-371-942-110	Sequence 110, App
23	92.4	66.0	125	17	US-10-371-942-118	Sequence 118, App
24	92.4	66.0	139	14	US-10-300-675-2	Sequence 2, Appli
25	92.4	66.0	139	17	US-10-910-124-2	Sequence 2, Appli
26	92.4	66.0	139	17	US-10-893-576-43	Sequence 43, Appl
27	92.4	66.0	142	17	US-10-484-790A-10	Sequence 10, Appl
28	92.4	66.0	223	10	US-09-972-656-66	Sequence 66, Appl
29	92.4	66.0	229	10	US-09-972-656-82	Sequence 82, Appl
30	92.4	66.0	230	10	US-09-972-656-72	Sequence 72, Appl
31	92.4	66.0	249	10	US-09-880-748-957	Sequence 957, App
32	92.4	66.0	249	15	US-10-293-418-957	Sequence 957, App
33	92.4	66.0	250	10	US-09-880-748-1413	Sequence 1413, Ap
34	92.4	66.0	250	15	US-10-293-418-1413	Sequence 1413, Ap
35	92.4	66.0	253	10	US-09-880-748-1333	Sequence 1333, Ap
36	92.4	66.0	253	15	US-10-293-418-1333	Sequence 1333, Ap
37	92.4	66.0	254	10	US-09-880-748-1659	Sequence 1659, Ap
38	92.4	66.0	254	15	US-10-293-418-1659	Sequence 1659, Ap
39	92.4	66.0	450	17	US-10-484-790A-17	Sequence 17, Appl
40	92.4	66.0	453	17	US-10-484-790A-18	Sequence 18, Appl
41	90.4	64.6	246	10	US-09-880-748-1847	Sequence 1847, Ap
42	90.4	64.6	246	15	US-10-293-418-1847	Sequence 1847, Ap
43	90.3	64.5	123	14	US-10-269-805-31	Sequence 31, Appl
44	90.3	64.5	123	14	US-10-269-805-55	Sequence 55, Appl
45	88.4	63.1	255	10	US-09-880-748-1642	Sequence 1642, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.:   3.33e-05   Length: 249
Score: 113.10   Matches: 26
Percent Similarity: 20.63%   Conservative: 0
Best Local Similarity: 20.63%   Mismatches: 1
Query Match: 80.79%   Indels: 99
DB: Gaps: 1

NOLAN463-1A.SEQ (1-81) x US-09-880-748-1321 (1-249)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGT------------ 48
            ||| |||||||||||||||||||||||||||| ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 -- 48
Db   70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89

Qy   48 -- 48
Db   90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109

Qy   48 -- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129

Qy   48 -- 48
Db 130 GlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGlnSerPro 149

Qy   49 ------------------------------------CGGGCGAGTCAGGAT 63
                                             ||||||||
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169

Qy   64 ATTAGCAGCTGGTTAGCC 81
           ||||||||
Db 170 IleSerSerTrpLeuAla 175

RESULT 2
US-10-293-418-1321
; Sequence 1321, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1321

Alignment Scores:
Pred. No.:   3.33e-05   Length: 249
Score: 113.10   Matches: 26
Percent Similarity: 20.63%   Conservative: 0
Best Local Similarity: 20.63%   Mismatches: 1
Query Match: 80.79%   Indels: 99
DB: 15   Gaps: 1

NOLAN463-1A.SEQ (1-81) x US-10-293-418-1321 (1-249)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGT------------ 48
            ||| |||||||||||||||||||||||||||| ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 -- 48
Db   70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89

Qy   48 -- 48
Db   90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109

Qy   48 -- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129

Qy   48 -- 48
Db 130 GlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGlnSerPro 149

Qy   49 ------------------------------------CGGGCGAGTCAGGAT 63
                                             ||||||||
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169

Qy   64 ATTAGCAGCTGGTTAGCC 81
           ||||||||
Db 170 IleSerSerTrpLeuAla 175

RESULT 3
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: GALIBERT, Laurent J.
; APPLICANT: YAN, Wei
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.:   0.00362   Length: 115
Score: 96.40   Matches: 19
Percent Similarity: 41.18%   Conservative: 2
Best Local Similarity: 37.25%   Mismatches: 4
Query Match: 68.86%   Indels: 26
DB: 17   Gaps: 1

```
NOLAN463-1A.SEQ (1-81) x US-10-898-408-12 (1-115)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||      :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMet 69

Qy   61 GATATTAGC--                                                  69
        :::
Db   70 SerValAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAsp 89

Qy   70 ---------------AGCTCGG 75
                       ||||||
Db   90 ThrAlaValTyrTyrCysAlaArgValSerTrp 100

RESULT 4
US-09-880-748-993
; Sequence 993, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-993

Alignment Scores:
Pred. No.:                0.00905              Length:          250
Score:                    93.80                Matches:         20
Percent Similarity:       80.77%               Conservative:    1
Best Local Similarity:    76.92%               Mismatches:      3
Query Match:              67.00%               Indels:          2
DB:                       10                   Gaps:            1

NOLAN463-1A.SEQ (1-81) x US-09-880-748-993 (1-250)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCG------ 54
        ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnProSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
        |||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75

RESULT 5
US-10-293-418-993
; Sequence 993, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
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; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-993

Alignment Scores:
Pred. No.:                0.00905              Length:          250
Score:                    93.80                Matches:         20
Percent Similarity:       80.77%               Conservative:    1
Best Local Similarity:    76.92%               Mismatches:      3
Query Match:              67.00%               Indels:          2
DB:                       15                   Gaps:            1

NOLAN463-1A.SEQ (1-81) x US-10-293-418-993 (1-250)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCG------ 54
        ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnProSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
        |||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75

RESULT 6
US-09-880-748-954
; Sequence 954, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-954

Alignment Scores:
Pred. No.:                0.00908              Length:          253
Score:                    93.80                Matches:         20
Percent Similarity:       80.77%               Conservative:    1
Best Local Similarity:    76.92%               Mismatches:      3
Query Match:              67.00%               Indels:          2
```

DB: 10   Gaps: 1

NOLAN463-1A.SEQ (1-81) x US-09-880-748-954 (1-253)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCG------ 54
          ||||||||||| ||||||||||||||||||||||||||||||||||||||| ||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
          ||||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75

RESULT 7
US-10-293-418-954
; Sequence 954, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-954

Alignment Scores:
Pred. No.:   0.00908   Length: 253
Score: 93.80   Matches: 20
Percent Similarity: 80.77%   Conservative: 1
Best Local Similarity: 76.92%   Mismatches: 3
Query Match: 67.00%   Indels: 2
DB: 15   Gaps: 1

NOLAN463-1A.SEQ (1-81) x US-10-293-418-954 (1-253)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCG------ 54
          ||||||||||| ||||||||||||||||||||||||||||||||||||||| ||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
          ||||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75

RESULT 8
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY

; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2

Alignment Scores:
Pred. No.:   0.0107   Length: 80
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 14   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-078-958-2 (1-80)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGGGAGTCAG 60
          ||||||||||| ||||||||||||||||||||||||||||||||||||||| :::
Db   33 GluIleAsnHisSerGlySerThrAsnProSerLeuLysSerArgValThr--- 51

Qy   61 GATATTAGC 69
          |||||
Db   52 ---IleSer 53

RESULT 9
US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US2003003649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40

Alignment Scores:
Pred. No.:   0.0112   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 14   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-194-975-40 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGGGAGTCAG 60
          ||||||||||| ||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 10

US-10-308-817-83
; Sequence 83, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-308-817-83

Alignment Scores:
Pred. No.:   0.0112   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 15   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-308-817-83 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          ||||||
Db   69 ---IleSer 70

RESULT 11
US-10-032-037B-87
; Sequence 87, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-87

Alignment Scores:
Pred. No.:   0.0112   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 15   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-032-037B-87 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          ||||||
Db   69 ---IleSer 70

Db   69 ---IleSer 70

RESULT 12
US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-87

Alignment Scores:
Pred. No.:   0.0112   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 15   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-029-988B-87 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG--- 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          ||||||
Db   69 ---IleSer 70

RESULT 13
US-10-032-423A-87
; Sequence 87, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.:   0.0112   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 15   Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-032-423A-87 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60

```
Db        50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy        61 GATATTAGC 69
             |||||
Db        69 ---IleSer 70
```

RESULT 14

US-10-453-698-83

```
; Sequence 83, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
;   APPLICANT: Rother, Russell
;   TITLE OF INVENTION: HYBRID ANTIBODIES
;   FILE REFERENCE: 82 CIP (1087-37 CIP)
;   CURRENT APPLICATION NUMBER: US/10/453,698
;   CURRENT FILING DATE:  2003-06-03
;   NUMBER OF SEQ ID NOS: 196
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: human
US-10-453-698-83
```

```
Alignment Scores:
Pred. No.:                 0.0112        Length:            97
Score:                     92.40         Matches:           19
Percent Similarity:        74.07%        Conservative:       1
Best Local Similarity:     70.37%        Mismatches:         1
Query Match:               66.00%        Indels:             6
DB:                        15            Gaps:               0
```

NOLAN463-1A.SEQ (1-81) x US-10-453-698-83 (1-97)

```
Qy         1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
             |||||||||||||||||||||||||||||||||||||||||||||||| ::: 
Db        50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy        61 GATATTAGC 69
             |||||
Db        69 ---IleSer 70
```

RESULT 15

US-10-029-926B-87

```
; Sequence 87, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
;   APPLICANT: HAGAY, et al.
;   TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
;   FILE REFERENCE: 10793/50
;   CURRENT APPLICATION NUMBER: US/10/029,926B
;   CURRENT FILING DATE:  2001-12-31
;   PRIOR APPLICATION NUMBER: 60/258,948
;   PRIOR FILING DATE: 12/29/2000
;   NUMBER OF SEQ ID NOS: 203
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-029-926B-87
```

```
Alignment Scores:
Pred. No.:                 0.0112        Length:            97
Score:                     92.40         Matches:           19
Percent Similarity:        74.07%        Conservative:       1
Best Local Similarity:     70.37%        Mismatches:         1
Query Match:               66.00%        Indels:             6
DB:                        15            Gaps:               0
```

NOLAN463-1A.SEQ (1-81) x US-10-029-926B-87 (1-97)

```
Qy         1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
             |||||||||||||||||||||||||||||||||||||||||||||||| ::: 
Db        50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy        61 GATATTAGC 69
             |||||
Db        69 ---IleSer 70
```

Search completed: August 4, 2005, 18:49:48
Job time : 87.25 secs

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     August  4, 2005, 18:04:24 ; Search time 18.25 Seconds
                              (without alignments)
                              854.089 Million cell updates/sec

Title:          NOLAN463-1A.SEQ
Perfect score:  140
Sequence:       1 GAAATCAATCATAGTGGAAG.......ATATTAGCAGCTGGTTAGCC  81

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext   0.1
                Ygapop 10.0 , Ygapext   0.1
                Fgapop  6.0 , Fgapext   0.1
                Delop   6.0 , Delext    0.1

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:       566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPRO_spool_p/NOLAN08728463-1/runat_04082005_125806_24544/app_query.fasta_1.5
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN 1 1 77 @runat_04082005_125806_24544 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :      PIR_79:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	67.1	97	2	S26806	Ig heavy chain V r
2	93.9	67.1	140	2	S78052	Ig heavy chain pre
3	92.4	66.0	97	2	S26898	Ig heavy chain V r
4	92.4	66.0	97	2	S26805	Ig heavy chain V r
5	92.4	66.0	106	2	S37454	Ig mu chain - huma
6	92.4	66.0	122	2	JL0047	Ig heavy chain V r
7	92.4	66.0	126	2	S47010	Ig heavy chain V4.
8	92.4	66.0	133	2	PS0341	Ig heavy chain V-D
9	92.4	66.0	140	2	A49045	Ig heavy chain V r
10	92.4	66.0	143	2	B49028	Ig heavy chain V-I
11	92.4	66.0	231	2	B23746	Ig Fab region IV-J
12	88.4	63.1	97	2	G34964	Ig heavy chain V-I
13	84.4	60.3	98	2	S26905	Ig heavy chain V r
14	83.4	59.6	97	2	S14474	Ig heavy chain V r

No.					ID	Description
15	81.4	58.1	129	2	S44114	Ig heavy chain V r
16	80.4	57.4	134	2	S54906	Ig heavy chain V r
17	80	57.1	123	2	S30529	Ig heavy chain V r
18	79.1	56.5	140	2	I37782	Ig variable region
19	78.4	56.0	98	2	S26904	Ig heavy chain V r
20	78.4	56.0	145	2	S78055	Ig heavy chain pre
21	78.4	56.0	146	1	G1HUH2	Ig heavy chain pre
22	77.3	55.3	114	2	I72667	cold agglutinin FS
23	77.3	55.2	130	2	S31673	Ig heavy chain V r
24	77	55.0	134	2	B24672	Ig heavy chain pre
25	75.4	53.9	97	2	JH0428	Ig gamma chain V r
26	74.4	53.1	106	2	S26464	Ig heavy chain V r
27	74	52.9	116	2	S38718	Ig heavy chain V r
28	73.4	52.4	97	2	S26906	Ig heavy chain V r
29	73.4	52.4	97	2	S12416	Ig heavy chain V r
30	73.4	52.4	99	2	S12412	Ig heavy chain V r
31	73.4	52.4	105	2	S44125	Ig lambda chain V
32	73.4	52.4	116	2	B26340	Ig heavy chain pre
33	73.4	52.4	118	2	A26340	Ig heavy chain pre
34	73.4	52.4	130	2	S31690	Ig heavy chain V r
35	73.1	52.2	127	2	S19668	Ig heavy chain V r
36	72	51.4	97	2	S26804	Ig heavy chain V r
37	72	51.4	97	2	S26808	Ig heavy chain V r
38	72	51.4	116	2	S18557	Ig heavy chain V r
39	72	51.4	137	2	S31676	Ig heavy chain V r
40	72	51.4	139	2	S31696	Ig heavy chain V r
41	72	51.4	139	2	S31586	Ig heavy chain V r
42	71.5	51.1	109	2	PH1673	Ig heavy chain V r
43	71.4	51.0	97	2	PL0118	Ig heavy chain V-I
44	71.4	51.0	98	2	S26902	Ig heavy chain V r
45	71.4	51.0	98	2	S12421	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S26806
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26806
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26806; MUID:92201299; PMID:1348029
A;Accession: S26806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.000964          Length:         97
Score:                  94.00             Matches:        17
Percent Similarity:     83.33%            Conservative:   3
Best Local Similarity:  70.83%            Mismatches:     4
Query Match:            67.14%            Indels:         0
DB:                     2                 Gaps:           0

NOLAN463-1A.SEQ (1-81) x S26806 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCCCTCAAGAGTCGGGCCAGTCAG  60
                                                              :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgIleThrMet  69

Qy   61 GATATTAGCAGC  72
          :::    :::
Db   70 SerValAspThr  73

RESULT 2
```

S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:　　　　　　　　0.00102　　　Length:　　　　140
Score:　　　　　　　　　　93.90　　　Matches:　　　21
Percent Similarity:　　33.85%　　　Conservative:　1
Best Local Similarity:　32.31%　　　Mismatches:　　2
Query Match:　　　　　　67.07%　　　Indels:　　　　41
DB:　　　　　　　　　　　　　　　　Gaps:　　　　　1

NOLAN463-1A.SEQ (1-81) x S78052 (1-140)

Qy　　1 GAAATCAATCATAGTGGAAGCAACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
　　　　　||||||||||||||||||||||||||||||||||||||||||||||　　:::
Db　 64 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 82

Qy　 61 GATATTAGC--- 69
　　　　　|||||||||
Db　 83 ---IleSerValAspThrSerLysAsnGlnPheSerLeuLysSerValThrAla 101

Qy　 70 --AGCTGG 75
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　||||
Db　102 AlaAspThrAlaValTyrTyrCysAlaArgGlyGlySerValLeuArgPheLeuGluTrp 121

Qy　 76 TTA 78
　　　　　|||
Db　122 Leu 122

RESULT 3
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898; S12420
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26898
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
A;Experimental source: clone DP-63
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12420

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <SAN>
A;Cross-references: EMBL:X56364
A;Experimental source: V(H)4.2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:　　　　　　　　0.00156　　　Length:　　　　97
Score:　　　　　　　　　　92.40　　　Matches:　　　19
Percent Similarity:　　74.07%　　　Conservative:　1
Best Local Similarity:　70.37%　　　Mismatches:　　1
Query Match:　　　　　　66.00%　　　Indels:　　　　6
DB:　　　　　　　　　　　　　　　　Gaps:　　　　　0

NOLAN463-1A.SEQ (1-81) x S26898 (1-97)

Qy　　1 GAAATCAATCATAGTGGAAGCAACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
　　　　　||||||||||||||||||||||||||||||||||||||||||||||　　:::
Db　 50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy　 61 GATATTAGC 69
　　　　　|||||
Db　 69 ---IleSer 70

RESULT 4
S26805
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
A;Accession: S26805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:　　　　　　　　0.00156　　　Length:　　　　97
Score:　　　　　　　　　　92.40　　　Matches:　　　19
Percent Similarity:　　74.07%　　　Conservative:　1
Best Local Similarity:　70.37%　　　Mismatches:　　1
Query Match:　　　　　　66.00%　　　Indels:　　　　6
DB:　　　　　　　　　　　　　　　　Gaps:　　　　　0

NOLAN463-1A.SEQ (1-81) x S26805 (1-97)

Qy　　1 GAAATCAATCATAGTGGAAGCAACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
　　　　　||||||||||||||||||||||||||||||||||||||||||||||　　:::
Db　 50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy　 61 GATATTAGC 69
　　　　　|||||
Db　 69 ---IleSer 70

RESULT 5
S37454
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from ｒ

A;Reference number: S37453
A;Accession: S37454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>
A;Cross-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Alignment Scores:
Pred. No.:   0.00157   Length: 106
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 2   Gaps: 0

NOLAN463-1A.SEQ (1-81) x S37454 (1-106)

Qy   1 GAAATCAATCATCATGTGGAAGCAGCACCAACTACAACCCGTCCTCAAGAGTCGGGCGAGTCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   28 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 46

Qy   61 GATATTAGC   69
           |||||
Db   47 ---IleSer   48

RESULT 6
JL0047
Ig heavy chain V region precursor (clone cR18) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: JL0047
R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5
A;Reference number: JL0047; MUID:88258392; PMID:3113445
A;Accession: JL0047
A;Molecule type: mRNA
A;Residues: 1-122 <BAE>
A;Experimental source: T-cell line RPMI 8402
A;Note: the authors translated the reading frame which extends to the stop codon; the se
A;Note: this sequence belongs to the VH II subgroup
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00159   Length: 122
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 2   Gaps: 0

NOLAN463-1A.SEQ (1-81) x JL0047 (1-122)

Qy   1 GAAATCAATCATCATGTGGAAGCAGCACCAACTACAACCCGTCCTCAAGAGTCGGGCGAGTCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   58 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 76

Qy   61 GATATTAGC   69
           |||||
Db   77 ---IleSer   78

RESULT 7
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S47010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994

A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A;Reference number: S47009
A;Accession: S47010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00159   Length: 126
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 2   Gaps: 0

NOLAN463-1A.SEQ (1-81) x S47010 (1-126)

Qy   1 GAAATCAATCATCATGTGGAAGCAGCACCAACTACAACCCGTCCTCAAGAGTCGGGCGAGTCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC   69
           |||||
Db   69 ---IleSer   70

RESULT 8
PS0341
Ig heavy chain V-D-J region (RAMOS) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C;Accession: PS0341
R;Ratechi, H.
Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
A;Reference number: PS0341; MUID:92171937; PMID:1540170
A;Accession: PS0341
A;Molecule type: mRNA
A;Residues: 1-133 <RAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-38/Region: framework 1
F;39-43/Region: complementarity-determining 1
F;44-57/Region: framework 2
F;58-74/Region: complementarity-determining 2
F;75-106/Region: framework 3

Alignment Scores:
Pred. No.:   0.0016   Length: 133
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 2   Gaps: 0

NOLAN463-1A.SEQ (1-81) x PS0341 (1-133)

Qy   1 GAAATCAATCATCATGTGGAAGCAGCACCAACTACAACCCGTCCTCAAGAGTCGGGCGAGTCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   58 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 76

Qy   61 GATATTAGC   69
           |||||
Db   77 ---IleSer   78

RESULT 9
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

```
C;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma
  Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <GRI>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.00161      Length:          140
Score:                  92.40        Matches:         19
Percent Similarity:     74.07%       Conservative:    1
Best Local Similarity:  70.37%       Mismatches:      1
Query Match:            66.00%       Indels:          6
DB:                     2            Gaps:            0

NOLAN463-1A.SEQ (1-81) x A49045 (1-140)

Qy    1 GAAATCAATCATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        |||||||||||||||||||||||||||||||||||||||||||||| |||  :::
Db   69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy   61 GATATTAGC 69
        |||||
Db   88 ---IleSer 89

RESULT 10
B49028
Ig heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
  Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: B49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-143 <TIM>
A;Cross-references: GB:S64473; NID:g236906; PIDN:AAB20012.1; PID:g236907
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.00161      Length:          143
Score:                  92.40        Matches:         19
Percent Similarity:     74.07%       Conservative:    1
Best Local Similarity:  70.37%       Mismatches:      1
Query Match:            66.00%       Indels:          6
DB:                     2            Gaps:            0

NOLAN463-1A.SEQ (1-81) x B49028 (1-143)

Qy    1 GAAATCAATCATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        |||||||||||||||||||||||||||||||||||||||||||||| |||  :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        |||||
Db   69 ---IleSer 70

RESULT 11
```

```
B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
  J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91111575; PMID:1993660
A;Accession: B23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.00167      Length:          231
Score:                  92.40        Matches:         19
Percent Similarity:     74.07%       Conservative:    1
Best Local Similarity:  70.37%       Mismatches:      1
Query Match:            66.00%       Indels:          6
DB:                     2            Gaps:            0

NOLAN463-1A.SEQ (1-81) x B23746 (1-231)

Qy    1 GAAATCAATCATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        |||||||||||||||||||||||||||||||||||||||||||||| |||  :::
Db   49 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 67

Qy   61 GATATTAGC 69
        |||||
Db   68 ---IleSer 69

RESULT 12
G34964
Ig heavy chain V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
  J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
A;Molecule type: mRNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.00524      Length:          97
Score:                  88.40        Matches:         18
Percent Similarity:     70.37%       Conservative:    1
Best Local Similarity:  66.67%       Mismatches:      2
Query Match:            63.14%       Indels:          6
DB:                     2            Gaps:            0

NOLAN463-1A.SEQ (1-81) x G34964 (1-97)

Qy    1 GAAATCAATCATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlyThrGlyThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        |||||
Db   69 ---IleSer 70

RESULT 13
S26905
Ig heavy chain v region (DP-70 / 4.19) - human (fragment)
```

```
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
  J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
  EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12419
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <SAN>
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.0176        Length:         98
Score:                  84.40         Matches:        18
Percent Similarity:     70.37%        Conservative:   1
Best Local Similarity:  66.67%        Mismatches:     2
Query Match:            60.29%        Indels:         6
DB:                     2             Gaps:           0

NOLAN463-1A.SEQ (1-81) x S26905 (1-98)

Qy    1 GAAATCAATCATAGTGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGGCAGTCAG 60
        |||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   51 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 69

Qy   61 GATATTAGC 69
        |||||
Db   70 ---IleSer 71

RESULT 14
S14474
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S14474
R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H
  submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Accession: S14474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <ESJ>
A;Cross-references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:g1335354
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.0238        Length:         97
Score:                  83.40         Matches:        18
Percent Similarity:     70.37%        Conservative:   1
Best Local Similarity:  66.67%        Mismatches:     2
Query Match:            59.57%        Indels:         6
DB:                     2             Gaps:           0

NOLAN463-1A.SEQ (1-81) x S14474 (1-97)

Qy    1 GAAATCAATCATAGTGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGGCAGTCAG 60
        |||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   50 GluIleIleHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        |||||
Db   69 ---IleSer 70

RESULT 15
S44114
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44114
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
  submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAW>
A;Cross-references: EMBL:Z31579; NID:g472968; PIDN:CAA83451.1; PID:g940525
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.0444        Length:         129
Score:                  81.40         Matches:        17
Percent Similarity:     67.86%        Conservative:   2
Best Local Similarity:  60.71%        Mismatches:     3
Query Match:            58.14%        Indels:         6
DB:                     2             Gaps:           0

NOLAN463-1A.SEQ (1-81) x S44114 (1-129)

Qy    1 GAAATCAATCATAGTGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGGCAGTCAG 60
        |||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   51 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerPheLysSerArgValThr--- 69

Qy   61 GATATTAGCAGC 72
        |||||:::
Db   70 ---IleSerAla 72

Search completed: August  4, 2005, 18:21:23
Job time : 20.25 secs
```

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```
              GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August  4, 2005, 17:55:57 ; Search time 83.75 Seconds
                                       (without alignments)
                         990.529 Million cell updates/sec

Title:      NOLAN463-1A.SEQ
Perfect score: 140
Sequence:   1 GAAATCAATCATAGTGGAAG.........ATATTAGCAGCTGGTTAGCC 81

Scoring table: BLOSUM62
           Xgapop 10.0 , Xgapext  0.1
           Ygapop 10.0 , Ygapext  0.1
           Fgapop  6.0 , Fgapext  0.1
           Delop   6.0 , Delext   0.1

Searched:   1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:  3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

```
Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-1/runat_04082005_125806_24533/app_query.fasta_1.5
-DB=UniProt -QMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN 1 1 305 @runat 04082005 125806 24533 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :   UniProt_03:*
          1: uniprot_sprot:*
          2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	92.4	66.0	116	2	Q7Z3Y6	Q7z3y6 homo sapien
2	92.4	66.0	595	2	Q8WUX4	Q8wux4 homo sapien
3	92.4	66.0	597	2	Q6GMX5	Q6gmx5 homo sapien
4	92.4	66.0	597	2	Q9BU10	Q9bu10 homo sapien
5	92.4	66.0	625	2	Q96AA6	Q96aa6 homo sapien
6	86.4	61.7	597	2	Q9BQB8	Q9bqb8 homo sapien
7	84.4	60.3	576	2	Q6P4I8	Q6p4i8 homo sapien
8	81.3	58.1	477	2	Q6GMX7	Q6gmx7 homo sapien
9	78.4	56.0	146	1	HV2I_HUMAN	P06331 homo sapien
10	73.7	52.6	139	2	Q86SX2	Q86sx2 homo sapien
11	72.6	51.9	479	2	Q99M22	Q99m22 mus musculu
12	72	51.4	465	2	Q6GMX6	Q6gmx6 homo sapien
13	72	51.4	620	2	Q96EY0	Q96ey0 homo sapien
14	70.6	50.4	262	2	Q65ZI1	Q65zi1 mus musculu
15	69.3	49.5	119	2	Q9UL73	Q9ul73 homo sapien
16	69.1	49.4	113	1	HV47_MOUSE	P01823 mus musculu
17	69	49.3	116	1	HV61_MOUSE	P18532 mus musculu
18	67.4	48.1	2348	2	Q82027	Q82027 anabaena sp
19	66.9	47.8	476	2	Q6GMX1	Q6gmx1 homo sapien
20	65	46.4	116	1	HV60_MOUSE	P18531 mus musculu
21	65	46.4	478	2	Q6NYH3	Q6nyh3 homo sapien
22	64	45.7	478	2	Q7Z379	Q7z379 homo sapien
23	60.8	43.4	3118	2	O17575	O17575 caenorhabdi
24	59.5	42.5	1160	2	TFC3_YEAST	P34111 saccharomyc
25	59.4	42.4	150	2	O95973	O95973 homo sapien
26 c	59.1	42.1	274	2	Q9FL48	Q9fl48 arabidopsis
27	59	42.1	136	2	Q6LBQ5	Q6lbq5 mus musculu
28	59	42.1	137	1	HV46_MOUSE	P01822 mus musculu
29	59	42.1	209	2	UPP_OCEIH	Q8xwu0 oceanobacil
30 c	58.7	41.9	209	2	Q8XWU0	Q8xwu0 ralstonia s
31	58.6	39.3	451	2	Q6NGD8	Q6ngd8 corynebacte
32 c	58.6	39.3	467	1	DPO4_CORGL	Q8nnp4 corynebacte
33	57.8	41.3	1083	1	KG88_HUMAN	Q9coh5 homo sapien
34	57.5	41.1	393	2	Q7WZ77	Q7wz77 nonomuraea
35	57.5	41.1	963	2	Q8P5M2	Q8p5m2 xanthomonas
36	57.4	41.0	496	2	Q96KX8	Q96kx8 homo sapien
37	57.2	40.9	729	1	DCMA_MOOTH	P27988 moorella th
38 c	57	38.3	337	2	Q6LOH3	Q610h3 picrophilus
39	57	40.7	1916	2	Q9VKG8	Q9vkg8 drosophila
40	56.6	40.5	212	2	Q926K5	Q926k5 listeria in
41	56.6	40.4	360	2	Q92UL5	Q92ul5 rhizobium m
42	56.6	40.4	408	1	YBX0_ARATH	Q8zq34 arabidopsis
43	56.4	40.3	390	2	Q6HH60	Q6hh60 bacillus th
44	56.4	40.3	545	2	Q6HH58	Q6hh58 bacillus th
45	56.4	40.3	588	2	Q813F9	Q813f9 bacillus ce

ALIGNMENTS

```
RESULT 1
Q7Z3Y6
ID   Q7Z3Y6        PRELIMINARY;      PRT;    116 AA.
AC   Q7Z3Y6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rearranged VH4-34 V gene segment (Fragment).
GN   Name=VH4-34;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564425; CAD92032.1; -.
DR   HSSP; P18532; 1KCV.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER         1      1
FT   NON_TER       116    116
SQ   SEQUENCE   116 AA;   12902 MW;  CE3D8A46616C908 CRC64;
```

```
Alignment Scores:
Pred. No.:               0.00339       Length:         116
Score:                   92.40         Matches:         19
Percent Similarity:      74.07%        Conservative:     1
Best Local Similarity:   70.37%        Mismatches:       1
Query Match:             66.00%        Indels:           6
DB:                      2             Gaps:             0

NOLAN463-1A.SEQ (1-81) x Q7Z3Y6 (1-116)

Qy   1 GAAATCAATCATAGTGGAAGCAACCGTCCCTCAAGAGTCGGGCGGAGTCAG  60
```

```
Db    50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
          |||||||||||||||||||||||||||||||||||||||||||||||||||||  :::

Qy    61 GATATTAGC 69
          |||||
Db    69 ---IleSer 70

RESULT 2
Q8WUX4
ID   Q8WUX4           PRELIMINARY;       PRT;   595 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019235; AAH19235.2; -.
     PIR; G34964; G34964.
     HSSP; P01861; 1ADQ.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Alignment Scores:
Pred. No.:               0.00426         Length:          595
Score:                   92.40           Matches:         19
Percent Similarity:      74.07%          Conservative:    1
Best Local Similarity:   70.37%          Mismatches:      1
Query Match:             66.00%          Indels:          6
DB:                                      Gaps:            0

NOLAN463-1A.SEQ (1-81) x Q8WUX4 (1-595)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   76 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 94
```

```
Qy    61 GATATTAGC 69
          |||||
Db    95 ---IleSer 96

RESULT 3
Q6GMX5
ID   Q6GMX5           PRELIMINARY;       PRT;   597 AA.
AC   Q6GMX5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073767; AAH73767.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Alignment Scores:
Pred. No.:               0.00427         Length:          597
Score:                   92.40           Matches:         19
Percent Similarity:      74.07%          Conservative:    1
Best Local Similarity:   70.37%          Mismatches:      1
Query Match:             66.00%          Indels:          6
DB:                                      Gaps:            0

NOLAN463-1A.SEQ (1-81) x Q6GMX5 (1-597)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
```

```
Db         ||||||| |||||||||||||||||||||||||||||||||||||| .::
        69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy      61 GATATTAGC 69
           ||||||
Db      88 ---IleSer 89


RESULT 4
Q9BU10
ID   Q9BU10           PRELIMINARY;     PRT;    597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human) .
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00407; IGc1; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Alignment Scores:
Pred. No.:                   0.00427        Length:            597
Score:                       92.40          Matches:            19
Percent Similarity:          74.07%         Conservative:        1
Best Local Similarity:       70.37%         Mismatches:          1
Query Match:                 66.00%         Indels:              6
DB:                          2              Gaps:                0

NOLAN463-1A.SEQ (1-81) x Q9BU10 (1-597)

Qy       1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
```

```
Qy      61 GATATTAGC 69
           ||||||
Db      88 ---IleSer 89


RESULT 5
Q96AA6
ID   Q96AA6           PRELIMINARY;     PRT;    625 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.2; -.
DR   PIR; S15590; S15590.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE 625 AA; 68610 MW; F62FAB3ADB7ECBFE CRC64;

Alignment Scores:
Pred. No.:                   0.00429        Length:            625
Score:                       92.40          Matches:            19
Percent Similarity:          74.07%         Conservative:        1
Best Local Similarity:       70.37%         Mismatches:          1
Query Match:                 66.00%         Indels:              6
DB:                          2              Gaps:                0

NOLAN463-1A.SEQ (1-81) x Q96AA6 (1-625)

Qy       1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
```

RESULT 6

```
                  |||||||||||||||||||||||||||||||||||||||||||  :::
Db    76 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 94

Qy    61 GATATTAGC 69
            ||||||
Db    95 ---IleSer 96
```

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ID   Q9BQB8
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
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Alignment Scores:

Pred. No.:	0.0281
Score:	86.40
Percent Similarity:	70.37%
Best Local Similarity:	66.67%
Query Match:	61.71%
DB:	2

Length:	597
Matches:	18
Conservative:	1
Mismatches:	2
Indels:	6
Gaps:	0

NOLAN463-1A.SEQ (1-81) x Q9BQB8 (1-597)

```
Qy     1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
           ||| || |||||| ||||| ||||  ||||||  |||||||||||||   :::
Db    69 GluIleAsnHisSerGlyIleThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
```

RESULT 7

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ID   Q6P4I8
AC   Q6P4I8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHD protein.
GN   Name=IGHD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063384; AAH63384.1; -.
DR   HSSP; P01820; 1A7N.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ   SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
```

Alignment Scores:

Pred. No.:	0.0524
Score:	84.40
Percent Similarity:	70.37%
Best Local Similarity:	66.67%
Query Match:	60.29%
DB:	2

Length:	576
Matches:	18
Conservative:	1
Mismatches:	2
Indels:	6
Gaps:	0

NOLAN463-1A.SEQ (1-576) x Q6P4I8 (1-576)

```
                  |||||||||||||||||||||||||||||||||||||||||||  :::
Db    76 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 94

Qy    61 GATATTAGC 69
            ||||||
Db    88 ---IleSer 89
```

NOLAN463-1A.SEQ (1-81) x Q6GMX7 (1-477)

```
Qy    4 ATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCGAGTCAGGAT 63
        ||||::|||||||||||||||||||| |||||||||||||||||||||||||||||  :::
Db   70 IleSerHisSerGlySerThrThrTyrAsnProSerLeuLysSerArgValThrLeuSer  89

Qy   64 ATT------------------------------------------------------------ 66
        :::
Db   90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109

Qy   67 ------------------------------------------------------AGCAGCTGG 75
                                                                ||||||
Db  110 AlaValTyrTyrCysAlaHisGlySerSerTrp 120
```

RESULT 9
HV2I_HUMAN

```
ID   HV2I_HUMAN            STANDARD;        PRT;    146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; GIHUH2.
DR   HSSP; P01825; 7FAB.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    146       Ig heavy chain V-II region ARH-77.
FT   DOMAIN       20    146       V segment.
FT   DOMAIN      118    127       D segment.
FT   DOMAIN      128    146       J segment.
FT   DISULFID     42    115       By similarity.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16228 MW;  8D7FD52BB218171F CRC64;
```

Alignment Scores:
```
Pred. No.:                    0.285                Length:           146
Score:                       78.40                 Matches:           17
Percent Similarity:          66.67%                Conservative:       1
Best Local Similarity:       62.96%                Mismatches:         3
Query Match:                 56.00%                Indels:             6
DB:                                                Gaps:               0
```

NOLAN463-1A.SEQ (1-81) x HV2I_HUMAN (1-146)

```
Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   70 GluIleAsnHisSerGlySerThrThrTyrTyrThrAsnTyrLysThrSerLeuLysSerArgValThr--- 88

Qy   61 GATATTAGC 69
        |||||||
Db   89 ---IleSer 90
```

RESULT 10
Q86SX2

(left column, earlier in reading order:)

```
Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCCCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   77 GluIleTyrHisSerGlySerThrAsnProSerLeuLysSerArgValThr-- 95

Qy   61 GATATTAGC 69
        |||||||
Db   96 ---IleSer 97
```

RESULT 8
Q6GMX7

```
ID   Q6GMX7          PRELIMINARY;      PRT;    477 AA.
AC   Q6GMX7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073765; AAH73765.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Hypothetical protein.
SQ   SEQUENCE   477 AA;  51631 MW;  9FE59C09C50CFF85 CRC64;
```

Alignment Scores:
```
Pred. No.:                    0.135                Length:           477
Score:                       81.30                 Matches:           17
Percent Similarity:          39.22%                Conservative:       3
Best Local Similarity:       33.33%                Mismatches:         4
Query Match:                 58.07%                Indels:            27
DB:                                                Gaps:               1
```

```
ID   Q86SX2          PRELIMINARY;      PRT;   139 AA.
AC   Q86SX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE   Homo sapiens (human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells.
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248300; CAD62627.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   139 AA;  15573 MW;  7D1E2302410E4F8C CRC64;
```

Alignment Scores:
Pred. No.:   1.24
Score: 73.70
Percent Similarity: 35.71%
Best Local Similarity: 30.36%
Query Match: 52.64%
DB: 2

NOLAN463-1A.SEQ (1-81) x Q86SX2 (1-139)

```
Qy    4 ATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGT------  57
          ::||||||||   ||||| ||| ||||||||||||||||||| :::
Db   83 IleTyrTyrSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIleSer 102

Qy   57 ------  57

Db  103 ValAspThrSerLysAsnGlnPheSerLeuSerSerSerValThrAlaAlaAspThr 122

Qy   58 ------CAGGATATTAGCAGC  72
              ||:::||||||
Db  123 AlaValTyrTyrCysAlaAlaArgAspThrValArgGlyValSerSer 138
```

RESULT 11

```
ID   Q99M22          PRELIMINARY;      PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  51992 MW;  768B39A138918892 CRC64;
```

Alignment Scores:
Pred. No.:   2.08
Score: 72.60
Percent Similarity: 33.93%
Best Local Similarity: 30.36%
Query Match: 51.86%
DB: 1

NOLAN463-1A.SEQ (1-81) x Q99M22 (1-479)

```
Qy    4 ATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCA----  59
          ||||||||   ||||| ||| ||||||||||||||||||||:::|||
Db   70 IleAsnTyrAspGlySerAsnAsnTyrAsnProSerLeuLysAsnArgIleSerIleThr  89

Qy   59 ------  59

Db   90 ArgAspThrSerLysAsnGlnPhePheLeuLysLeuAsnSerValThrGluAspThr 109

Qy   60 ------GGATATTAGCAGCTGG  75
              ||||||  |||||
Db  110 AlaThrTyrTyrCysAlaSerArgGlyTyr----SerTrp 121
```

RESULT 12

```
ID   Q6GMX6          PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

Left column

```
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;
```

Alignment Scores:

Pred. No.:	2.5	Length:	465
Score:	72.00	Matches:	13
Percent Similarity:	80.00%	Conservative:	3
Best Local Similarity:	65.00%	Mismatches:	4
Query Match:	51.43%	Indels:	0
DB:	2	Gaps:	0

```
NOLAN463-1A.SEQ (1-81) x Q6GMX6 (1-465)

Qy   13 AGTGGAAGCACCAACTACAACCGTCCTCAAGAGTCGGGCGAGTCAGGGATATTAGCAGC 72
            :::  :::  :::        :::        :::        :::  :::
Db   73  SerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMetSerValAspThr 92

RESULT 13
Q96EY0
ID   Q96EY0       PRELIMINARY;      PRT;   620 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
```

Right column

```
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.2; -.
DR   PIR; S15590; S15590.
DR   HSSP; P01820; 1GJ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   620 AA;  68125 MW;  990A1A4A6B8FF27B CRC64;
```

Alignment Scores:

Pred. No.:	2.61	Length:	620
Score:	72.00	Matches:	13
Percent Similarity:	80.00%	Conservative:	3
Best Local Similarity:	65.00%	Mismatches:	4
Query Match:	51.43%	Indels:	0
DB:	2	Gaps:	0

```
NOLAN463-1A.SEQ (1-81) x Q96EY0 (1-620)

Qy   13 AGTGGAAGCACCAACTACAACCGTCCTCAAGAGTCGGGCGAGTCAGGGATATTAGCAGC 72
            :::  :::  :::        :::        :::        :::  :::
Db   80  SerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMetSerValAspThr 99

RESULT 14
Q65ZI1
ID   Q65ZI1       PRELIMINARY;      PRT;   262 AA.
AC   Q65ZI1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Anti-HIV-1 reverse transcriptase single-chain variable.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hybridoma;
RX   MEDLINE=9621469; PubMed=8648670;
RA   Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
RT   "Targeting human immunodeficiency virus type 1 reverse transcriptase
RT   by intracellular expression of single-chain variable fragments to
RT   inhibit early stages of the viral life cycle.";
RL   J. Virol. 70:3392-3400(1996).
DR   EMBL; U48716; AAB64342.1; -.
```

```
DR   GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   RNA-directed DNA polymerase.
SQ   SEQUENCE   262 AA;  27842 MW;  7DF2013E53865E4 CRC64;

Alignment Scores:
Pred. No.:                    3.59
Score:                       70.60
Percent Similarity:          68.00%
Best Local Similarity:       64.00%
Query Match:                 50.43%
DB:                              2

NOLAN463-1A.SEQ (1-81) x Q65ZI1 (1-262)

Qy      4 ATCAATCATAGTGGAAGCAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAGGAT 63
          |||||||||:||||||||  |  |||||||||||||||||||||||||||||||||   || ||
Db    198 IleAsnTyrSerGlyAspThrTyrTyrTyrAsnProSerLeuLysSerArgIleSer----Il 216

Qy     64 ATTAGCA 70
          |   |||
Db    216 eThrAla 218
```

```
RESULT 15
Q9UL73
ID   Q9UL73          PRELIMINARY;      PRT;   119 AA.
AC   Q9UL73;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035041; AAD56277.1; -.
DR   PIR; PH0876; PH0876.
DR   PIR; S12416; S12416.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13219 MW;  1BDB6B6420EAOBE CRC64;

Alignment Scores:
Pred. No.:                    4.84
Score:                       69.30
Percent Similarity:          37.25%
Best Local Similarity:       29.41%
Query Match:                 49.50%
DB:                              2

NOLAN463-1A.SEQ (1-81) x Q9UL73 (1-119)
```

```
Qy      4 ATCAATCATAGTGGAAGCAGCACCAACTACAACCGTCCCTCAAGAGTCGGGCGAGTCAGGAT 63
            :::|||:|||||||  |  |||||||||||||||||||  :::
Db     51 IleTyrTyrSerGlySerThrAsnTyrThrProSerLeuLysSerArgValThrIleSer 70

Qy     64 ATT------------------------------------------------- 66
          :::
Db     71 ValAspArgSerLysAsnGlnPheSerLeuLysLeuThrSerLeuThrAlaAlaAspThr 90

Qy     67 -----------------------------------AGCAGCTGG 75
                                               |||:::|||
Db     91 AlaValTyrPheCysAlaArgLeuSerAsnTrp 101
```

```
Search completed: August  4, 2005, 18:20:06
Job time : 89.75 secs
```

```
                GenCore version 5.1.6
       Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:   August  4, 2005, 17:55:32 ; Search time 92.5 Seconds
                                       (without alignments)
                                  677.353 Million cell updates/sec

Title:           NOLAN463-1B.SEQ
Perfect score:   140
Sequence:        1 CGGGCGAGTCAGGATATTAG........ACAACCCGTCCCTCAAGAGT 81

Scoring table:   BLOSUM62

                 Xgapop  10.0 , Xgapext   0.1
                 Ygapop  10.0 , Ygapext   0.1
                 Fgapop   6.0 , Fgapext   0.1
                 Delop    6.0 , Delext    0.1

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Searched:        2105592 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:    4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Command line parameters:
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-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-1/runat_04082005_125805_24527/app_query.fasta_1.5
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN_1_1_308 @runat_04082005_125805_24527 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
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Database :  A_Geneseq_16Dec04:*
          1: geneseqp1980s:*
          2: geneseqp1990s:*
          3: geneseqp2000s:*
          4: geneseqp2001s:*
          5: geneseqp2002s:*
          6: geneseqp2003as:*
          7: geneseqp2003bs:*
          8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	100.1	71.5	253	5	ABP45322	Abp45322 Human Bly
2	100.1	71.5	253	7	ADG96149	Adg96149 Single ch
3	99.9	71.4	125	6	ADA89274	Ada89274 Human ant
4	98.2	70.1	80	2	AAW62794	Aaw62794 Amino aci
5	98.2	70.1	97	5	AAY05694	Aay05694 Multiple
6	98.2	70.1	97	5	ABG78212	Abg78212 Human Fv
7	98.2	70.1	97	5	ABG91903	Abg91903 Human ant
8	98.2	70.1	97	6	ABO27107	Abo27107 Human ger
9	98.2	70.1	97	7	ADB75646	Adb75646 Human pro
10	98.2	70.1	97	7	ADD28104	Add28104 Lymphoma
11	98.2	70.1	97	7	ADF10048	Adf10048 VEGF anti
12	98.2	70.1	97	7	ADF10150	Adf10150 Antibody
13	98.2	70.1	97	7	ADF09942	Adf09942 Antibody
14	98.2	70.1	97	7	ADJ80323	Adj80323 VH gene 1
15	98.2	70.1	114	3	AAB01949	Aab01949 Anti-Id1
16	98.2	70.1	114	3	AAB01950	Aab01950 Anti-Id1
17	98.2	70.1	114	3	AAB01953	Aab01953. Anti-Id1
18	98.2	70.1	114	3	AAB01959	Aab01959 High affi
19	98.2	70.1	114	3	AAB01952	Aab01952 Anti-Id1
20	98.2	70.1	114	3	AAB01955	Aab01955 Strepativ
21	98.2	70.1	114	3	AAB01956	Aab01956 Strepativ
22	98.2	70.1	114	3	AAB01948	Aab01948 Wild-type
23	98.2	70.1	114	3	AAB01954	Aab01954 Anti-Id1
24	98.2	70.1	114	7	ADG70086	Adg70086 Diversifi
25	98.2	70.1	114	7	ADG70013	Adg70013 Diversifi
26	98.2	70.1	116	2	AAR66324	Aar66324 Human imm
27	98.2	70.1	117	4	AAM60904	Aam60904 Human bra
28	98.2	70.1	117	4	ABG55317	Abg55317 Human liv
29	98.2	70.1	117	5	ABG43454	Abg43454 Human pep
30	98.2	70.1	118	2	ADA89246	Ada89246 Human ant
31	98.2	70.1	122	7	ADK17418	Adk17418 Anti-huma
32	98.2	70.1	122	8	ADG42840	Adg42840 scFv Ab12
33	98.2	70.1	123	7	AAW03757	Aaw03757 Anti-rhes
34	98.2	70.1	125	6	ADA89266	Ada89266 Human ant
35	98.2	70.1	139	3	AAY99556	Aay99556 Human LH1
36	98.2	70.1	139	7	ABR42859	Abr42859 Tumour-sp
37	98.2	70.1	139	7	ABW02445	Abw02445 Human mon
38	98.2	70.1	142	6	ABP96287	Abp96287 Anti-hTNF
39	98.2	70.1	154	6	ABP96293	Abp96293 Human ant
40	98.2	70.1	190	2	AAY34304	Aay34304 IgM antib
41	98.2	70.1	202	2	AAY34303	Aay34303 IgM antib
42	98.2	70.1	205	2	AAY34299	Aay34299 IgM antib
43	98.2	70.1	218	7	ADG70090	Adg70090 Diversifi
44	98.2	70.1	223	7	ADJ32112	Adj32112 Human int
45	98.2	70.1	224	7	ADG70088	Adg70088 Diversifi

ALIGNMENTS

```
RESULT 1
ABP45322
ID   ABP45322 standard; protein; 253 AA.
XX
AC   ABP45322;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1333.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO20020202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
```

PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1993-1994; 3140pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 253 AA;
XX
     Alignment Scores:
     Pred. No.:   0.000635   Length: 253
     Score: 100.10   Matches: 21
     Percent Similarity: 50.00%   Conservative: 0
     Best Local Similarity: 47.73%   Mismatches: 3
     Query Match: 71.50%   Indels: 19
     DB: Gaps: 5

NOLAN463-1B.SEQ (1-81) x ABP45322 (1-253)

Qy   3 GGCGAGTCA--GGATAT 17
        |||||||| ||||||
Db   26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy   18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA 77
        |||| ||:::: |||||||||||||||||||||||||||||||||||||||||||||
Db   46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
        ||||
Db   64 sSer 65

RESULT 2
ADG96149
ID   ADG96149 standard; protein; 253 AA.
XX
AC   ADG96149;
XX
DT   11-MAR-2004 (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 1333.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO200305979-A2.
XX
PD   10-JUL-2003.
XX

PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 1333; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ   Sequence 253 AA;
XX
     Alignment Scores:
     Pred. No.:   0.000635   Length: 253
     Score: 100.10   Matches: 21
     Percent Similarity: 50.00%   Conservative: 1
     Best Local Similarity: 47.73%   Mismatches: 3
     Query Match: 71.50%   Indels: 19
     DB: Gaps: 1

NOLAN463-1B.SEQ (1-81) x ADG96149 (1-253)

Qy   3 GGCGAGTCA--GGATAT 17
        |||||||| ||||||
Db   26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy   18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA 77
        |||| || |||||||||||||||||||||||||||||||||||||||||||
Db   46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
        ||||
Db   64 sSer 65

RESULT 3
ADA89274
ID   ADA89274 standard; protein; 125 AA.
XX
AC   ADA89274;
XX
DT   20-NOV-2003 (first entry)
XX
DE   Human antibody 3H2 heavy chain amino acid sequence SEQ ID NO:118.

```
Qy           25 -------------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACCCGTC 71
                            |||::: ||||||||||||||||||||||||||||||||||||
Db           44 yIleGlyGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64

Qy           72 CCTCAAGAGT 81
                ||||||||||
Db           64 rLeuLysSer 67

RESULT 4
AAW62794
ID   AAW62794 standard; peptide; 80 AA.
XX
AC   AAW62794;
XX
DT   23-SEP-1998  (first entry)
XX
DE   Amino acid sequence of a human antibody fragment.
XX
KW   Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW   inactivated endogenous Ig locus; B-cell development;
KW   human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW   kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW   production; antibody.
XX
OS   Homo sapiens.
XX
PN   WO9824893-A2.
XX
PD   11-JUN-1998.
XX
PF   03-DEC-1997;  97WO-US023091.
XX
PR   03-DEC-1996;  96US-00759620.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX
DR   WPI; 1998-333314/29.
XX
PT   New transgenic non-human mammals - having an inactivated immunoglobulin
PT   locus and a near complete human immunoglobulin locus, used for production
PT   of human antibodies.
XX
PS   Disclosure; Page 71; 128pp; English.
XX
CC   AAW62793-822 represent fragments of human antibodies produced by
CC   transgenic Xenomice, created using the method of the invention. The
CC   specification describes a transgenic non-human mammal which has genome
CC   modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC   locus, so that the mammal does not display normal B-cell development. The
CC   modified genome also has an inserted human heavy chain Ig locus in
CC   germline configuration, the human heavy chain Ig locus comprising a human
CC   micro constant region and regulatory and switch sequences, human J-H
CC   genes, human D-H genes, and human V-H genes and an inserted human kappa
CC   light chain Ig locus in germline configuration, the human kappa light
CC   chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC   and V-kappa genes, where the number of V-H and V-kappa genes inserted are
CC   selected to restore normal B-cell development in the mammal. The
CC   transgenic animals have a near complete human Ig locus, including both a
CC   human heavy chain locus and a human kappa light chain locus. They can be
CC   used for the production of human antibodies when exposed to particular
CC   antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC   will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
SQ   Sequence 80 AA;

Alignment Scores:
Pred. No.:              0.000842         Length:              80
Score:                  98.20            Matches:             19
Percent Similarity:     65.62%           Conservative:         2
Best Local Similarity:  59.38%           Mismatches:           3
```

```
XX
KW   immunoglobulin; Ig; heavy chain variable domain;
KW   light chain variable domain; major histocompatibility complex; MHC;
KW   gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW   cancer.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003070752-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003; 2003WO-US005128.
XX
PR   20-FEB-2002; 2002US-0358994P.
XX
PA   (DYAX-) DYAX CORP.
PA   (TECR ) TECHNION RES & DEV FOUND LTD.
XX
PI   Hoogenboom HRJM, Reiter Y;
XX
DR   WPI; 2003-663847/62.
DR   N-PSDB; ADA89273.
XX
PT   New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT   and an immunoglobulin light chain variable (VL) domain, useful for
PT   preparing a composition for treating or preventing a cancerous disorder.
XX
PS   Disclosure; Fig 28B; 224pp; English.
XX
CC   The present invention describes a protein comprising a protein comprising an immunoglobulin
CC   (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC   domain. The protein binds a complex comprising a major histocompatibility
CC   complex (MHC) and a peptide, does not substantially bind the MHC in the
CC   absence of the bound peptide, and does not substantially bind the peptide
CC   in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC   MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC   comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC   comprising one or more nucleic acids for expressing the Ig that binds a
CC   complex having an MHC and a peptide, does not substantially bind the MHC
CC   in the absence of the bound peptide, and does not substantially bind the
CC   peptide in the absence of the MHC; (3) an isolated nucleic acid
CC   comprising a first segment that encodes the Ig variable domain; (4) a
CC   host cell comprising heterologous nucleic acid sequences that encodes the
CC   novel protein; (5) a transgenic animal whose genome includes heterologous
CC   nucleic acid sequences that encode the protein; (6) identifying the
CC   protein that specifically encode the MHC-peptide complex; (7) expressing
CC   an antigen-binding protein; (8) ablating or killing a target cell that
CC   displays a peptide on a surface MHC molecule; (9) treating or preventing
CC   a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC   complex in a sample. A protein of the invention has cytostatic activity,
CC   and can be used in gene therapy. The protein is useful for preparing a
CC   composition for treating or preventing a cancerous disorder. The present
CC   sequence represents the heavy chain of an antibody which binds to an MHC-
CC   peptide complex where the peptide component in as peptide fragment of
CC   hTERT.
XX
SQ   Sequence 125 AA;

Alignment Scores:
Pred. No.:              0.000565         Length:             125
Score:                  99.90            Matches:             22
Percent Similarity:     50.00%           Conservative:         1
Best Local Similarity:  47.83%           Mismatches:           2
Query Match:            71.36%           Indels:              21
DB:                                      Gaps:                 1
```

```
NOLAN463-1B.SEQ (1-81) x ADA89274 (1-125)

Qy      3 GGCGAGTCAGGATATTAGCAGC------------------------------ 24
          |||    ||| ||||||||||||
Db     26 GlyGlySer----IleSerSerSerTyrTyrAlaTrpIleArgGlnProProGl 44
```

```
Query Match:        70.14%      Indels:         8              PR   19-SEP-1997;    97CA-02216595.
DB:                 2           Gaps:           0              PR   04-NOV-1997;    97CA-0222245.
                                                               XX
NOLAN463-1B.SEQ (1-81) x AAW62794 (1-80)                       PA   (QINY/) QIN Y.
                                                               XX
Qy     2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61    PI   Qin Y;
          |||::|       |||::|   ||||||||||||||||||||||||||||||          XX
Db    25  GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 42    DR   WPI; 1999-276985/23.
                                                               DR   N-PSDB; AAX25318.
Qy    62  ACAACCCGTCCCTCAAGAGT 81                                 XX
          ||||||||||||||||||                                     PT   Determination of B-cell clonality by amplification or enzymatic
Db    42  yrAsnProSerLeuLysSer 48                                     digestion.
                                                               XX
RESULT 5                                                        PS   Disclosure; Fig 9D; 67pp; English.
AAY05694                                                        XX
ID   AAY05694 standard; protein; 97 AA.                         CC   This sequence represents a heavy chain variable region (VH) as predicted
XX                                                              CC   from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
AC   AAY05694;                                                  CC   fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
XX                                                              CC   B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
DT   19-JUL-1999  (first entry)                                 CC   in nucleotide and predicted amino acid (see AAY05691-94) sequences were
XX                                                              CC   compared with the closest known germline VH genes; for 4d76, this was RA.
DE   Multiple sclerosis patient CSF B-cell VH region (clone 4d76).  CC   The results provided direct evidence that intrathecal clonally expanded B
XX                                                              CC   -cells from the CSF of MS patients are hypermutated postgerminal centre
KW   Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;      CC   antibody-forming or memory lymphocytes that have undergone antigen
KW   heavy chain variable region; VH gene; somatic hypermutation;  CC   selection. This finding implicates an important pathogenic pathway for
KW   B-cell clonality; RA gene; diagnosis; human.               CC   the development of demyelination in CNS of MS. The invention provides
XX                                                              CC   assay kits for determining B-cell or T-cell clonality. This technology
OS   Homo sapiens.                                              CC   allows the establishment of clonal specific RNA library from pathogenic
XX                                                              CC   cells in the CNS of patients, which is important for further
FH   Key            Location/Qualifiers                         CC   understanding of the role of antigen(s) in the cause of B-cell clonal
FT   Region         1..30                                       CC   expansion, and towards developing antigen specific therapeutic strategy
FT                  /label= FR1                                 XX
FT   Misc-difference 8                                          SQ   Sequence 97 AA;
FT                  /note= "encoded by GGC"
FT   Misc-difference 13                                         Alignment Scores:
FT                  /note= "replaces Glu of RA"                 Pred. No.:          0.000883           Length:              97
FT   Misc-difference 14                                         Score:              98.20              Matches:             19
FT                  /note= "encoded by CCT"                     Percent Similarity: 65.62%             Conservative:         2
FT   Misc-difference 23                                         Best Local Similarity: 59.38%          Mismatches:           3
FT                  /note= "replaces Gly of RA"                 Query Match:        70.14%             Indels:               8
FT   Misc-difference 25                                         DB:                 2                  Gaps:                 0
FT                  /note= "replaces Phe of RA"
FT   Misc-difference 30                                         NOLAN463-1B.SEQ (1-81) x AAY05694 (1-97)
FT                  /note= "replaces Gly of RA"
FT   Region         31..36                                      Qy     2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
FT                  /label= CDR1                                          |||::|       ||   |||::|   |||||||||||||||||||||||
FT   Misc-difference 31                                         Db    42  GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
FT                  /note= "replaces Gly of RA"
FT   Misc-difference 32                                         Qy    62  ACAACCCGTCCCTCAAGAGT 81
FT                  /note= "replaces Phe of RA"                           ||||||||||||||||||
FT   Region         37..50                                      Db    59  yrAsnProSerLeuLysSer 65
FT                  /label= FR2
FT   Region         51..66                                      RESULT 6
FT                  /label= CDR2                                 ABG78212
FT   Misc-difference 56                                         ID   ABG78212 standard; protein; 97 AA.
FT                  /note= "replaces Asn of RA"                  XX
FT   Misc-difference 57                                         AC   ABG78212;
FT                  /note= "replaces Ser of RA"                  XX
FT   Misc-difference 58                                         DT   15-NOV-2002  (first entry)
FT                  /note= "replaces Lys of RA"                  XX
FT   Region         67..97                                      DE   Human Fv molecule hypervariable region related peptide #87.
FT                  /label= FR3                                  XX
FT   Misc-difference 71                                         KW   Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
FT                  /note= "replaces Leu of RA"                  KW   disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
FT   Misc-difference 81                                         KW   lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
FT                  /note= "replaces Arg of RA"                  XX
XX                                                              OS   Homo sapiens.
PN   WO9915696-A1.                                              XX
XX                                                              PN   WO200259264-A2.
PD   01-APR-1999.                                               XX
XX                                                              PD   01-AUG-2002.
PF   17-SEP-1998;  98WO-CA000873.                               XX
XX                                                              PF   31-DEC-2001; 2001WO-US049440.
```

```
XX
PR   29-DEC-2000; 2000US-0751181.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI   Plaksin D, Peretz T;
XX
DR   WPI; 2002-619166/66.
XX
PT   Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT   or fragment, or construct of fragment with enhanced binding
PT   characteristics so as to selectively bind target cell in favor of other
PT   cells.
XX
PS   Claim 13; Page 193; 232pp; English.
XX
CC   The invention relates to a peptide or polypeptide comprising an Fv
CC   molecule, a construct or fragments or a construct of a fragment with
CC   enhanced binding characteristics which selectively and/or specifically
CC   binds to a target cell in favour of other cells, where binding is
CC   primarily determined by a first hypervariable region and Fv is a single
CC   chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC   association with or attached, coupled, combined, linked or fused to a
CC   pharmaceutical agent, is useful in the manufacture of a medicament, where
CC   the medicament has activity against a diseased cell, preferably a cancer
CC   cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC   myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC   acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC   composition for use in inhibiting the growth of a diseased or cancer
CC   cell. This sequence represents a human Fv molecule hypervariable region
CC   related peptide of the invention
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.000883      Length:            97
Score:                  98.20         Matches:           19
Percent Similarity:     65.62%        Conservative:      2
Best Local Similarity:  59.38%        Mismatches:        3
Query Match:            70.14%        Indels:            8
DB:                     5             Gaps:              0

NOLAN463-1B.SEQ (1-81) x ABG78212 (1-97)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         |||||||  ||       ||:::  |||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCCCTCAAGAGT 81
         ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 7
ABG91903
ID   ABG91903 standard; protein; 97 AA.
XX
AC   ABG91903;
XX
DT   04-DEC-2002 (first entry)
XX
DE   Human antibody fragment #87.
XX
KW   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW   metastasis; hypervariable region; autoimmune disease; thrombosis;
KW   restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW   myocardial infarction; retinopathic disease; abnormal platelet function;
KW   sulphated tyrosine-dependent protein-protein interaction.
XX
OS   Homo sapiens.
XX
PN   WO200253700-A2.
XX
```

```
XX
PD   11-JUL-2002.
XX
PF   31-DEC-2001; 2001WO-US049442.
XX
PR   29-DEC-2000; 2000US-0751181.
PR   29-DEC-2000; 2000US-0258948P.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI   Szanthon E, Richter T, Amit B, Kopperman L, Peretz T, Levanon A;
XX
DR   WPI; 2002-674776/72.
XX
PT   Novel isolated epitope present on cancer cells and important in
PT   physiological phenomena such as cell rolling, metastasis and
PT   inflammation, for treating autoimmune, inflammatory or cardiovascular
PT   diseases, and cancer.
XX
PS   Disclosure; Page 269; 0pp; English.
XX
CC   The invention relates to an isolated epitope present on cancer cells and
CC   important in physiological phenomena such as cell rolling, metastasis and
CC   inflammation, where the epitope is capable of being bound by an antibody,
CC   its antigen-binding fragment or its complex comprising at least one
CC   antibody or its binding fragment having a first hypervariable region. The
CC   epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC   disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC   tumour or leukaemia cells, increase in number of tumour or leukaemia
CC   cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC   platelet and/or cell-platelet adhesion or aggregation, for increasing
CC   mortality of tumour or leukaemia cells, for increasing the susceptibility
CC   of diseased cells to damage by anti-disease, anti-cancer or anti-
CC   leukaemia agents, or for decreasing the number of tumour or leukaemia
CC   cells in a patient, or in the manufacture of a medicament for the above
CC   mentioned purposes. The epitopes are useful for diagnosing and treating
CC   diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC   diseases, cardiovascular diseases such as myocardial infarction,
CC   retinopathic diseases and other diseases mediated by abnormal platelet
CC   function and diseases caused by sulphated tyrosine-dependent protein-
CC   protein interactions. This sequence represents a human antibody fragment
CC   of the invention
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.000883      Length:            97
Score:                  98.20         Matches:           19
Percent Similarity:     65.62%        Conservative:      2
Best Local Similarity:  59.38%        Mismatches:        3
Query Match:            70.14%        Indels:            8
DB:                     5             Gaps:              0

NOLAN463-1B.SEQ (1-81) x ABG91903 (1-97)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         |||||||  ||       ||:::  |||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCCCTCAAGAGT 81
         ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 8
ABG27107
ID   ABG27107 standard; protein; 97 AA.
XX
AC   ABG27107;
XX
DT   10-SEP-2003 (first entry)
XX
DE   Human germline heavy chain variable region gene segment #40.
XX
```

KW   Human; heavy chain variable region; VH; humanised antibody;
KW   chimeric antibody; complementarity determining region; CDR;
KW   canonical CDR structure type.
XX
OS   Homo sapiens.
XX
PN   US200303969-A1.
XX
PD   27-FEB-2003.
XX
PF   12-JUL-2002; 2002US-00194975.
XX
PR   12-JUL-2001; 2001US-0305111P.
XX
PA   (FOOT/) FOOTE J.
XX
PI   Foote J;
XX
DR   WPI; 2003-492151/46.
XX
PT   Making humanized antibody for converting antibody, by making chimeric
PT   antibodies containing complementarity determining region from non-human
PT   antibody and appropriate framework sequences of human antibodies.
XX
PS   Example 1; Fig 1; 31pp; English.
XX
CC   The invention describes a method of making a humanised antibody,
CC   comprising making chimeric antibodies containing a complementarity
CC   determining region (CDR) from a non-human antibody and appropriate
CC   framework sequences (I) of human antibodies. (I) is selected by using
CC   canonical CDR structure types of non-human antibody in comparison to
CC   germline canonical CDR structure types of human antibodies as the basis
CC   for selection, for humanisation. The method is useful for making a
CC   humanised antibody or a converted antibody. The method is applicable for
CC   converting a subject antibody sequence of any subject species to a less
CC   immunogenic form suitable for use in an object species. The method is
CC   reliable for identifying suitable human framework sequences to support
CC   non-human CDR regions and to provide humanised antibodies that retain
CC   high antigen binding with low immunogenicity in humans, without the need
CC   for direct comparison of framework sequences, without the need for
CC   determining critically important amino acid residues in the framework,
CC   and without the need for multiple iteration and construction to obtain
CC   humanised antibodies with suitable therapeutic properties. The antibody
CC   has high affinity and low immunogenicity without need for comparing
CC   framework sequences between non-human and human antibodies. This sequence
CC   represents a human heavy chain variable region gene segment used in the
CC   creation of humanised antibodies
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.000883   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 6   Gaps: 0

NOLAN463-1B.SEQ (1-81) x AB027107 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
            |||::: ||| |||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCGTCCCTCAAGAGT 81
          |||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 9
ADB75646
ID   ADB75646 standard; protein; 97 AA.
XX
AC   ADB75646;

XX
DT   04-DEC-2003   (first entry)
XX
DE   Human protein relating to the invention SEQ ID NO:55.
XX
KW   antibody library; CD1 region; CD2 region; VH region; VL region;
KW   immunoglobulin; CD3 region; TM1 scFv; human.
XX
OS   Homo sapiens.
XX
PN   WO200304198-A1.
XX
PD   30-MAY-2003.
XX
PF   22-NOV-2002; 2002WO-JP012236.
XX
PR   22-NOV-2001; 2001JP-00358602.
XX
PA   (UYKE-) UNIV KEIO.
XX
PI   Shimizu N, Takayanagi A, Okui M;
XX
DR   WPI; 2003-449818/42.
XX
PT   Highly stable artificial antibody libraries with super-repertory and
PT   little contamination from unexpressible ones, useful as tool in
PT   proteomics and e.g. for diagnosis and treating various diseases.
XX
PS   Disclosure; Page 101; 108pp; Japanese.
XX
CC   The invention relates to a novel artificial single-stranded antibody
CC   library with superior-repertory. The library is created by using a cDNA
CC   library as template for amplifying a fragment containing the CD1 and CD2
CC   regions of the VH or VL region of immunoglobulin gene and a fragment
CC   containing the CD3 region by PCR, respectively, producing VH and VL
CC   libraries, transferring into a host, and displaying the single-stranded
CC   antibody on a phage surface. An antibody library of the invention is
CC   useful as a tool in proteomics and antibody chips and filters, for
CC   screening ligands for antigens, and for studying protein-DNA interaction,
CC   diagnosis and treating various diseases. The present sequence represents
CC   a protein of the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.000883   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 7   Gaps: 0

NOLAN463-1B.SEQ (1-81) x ADB75646 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
            |||::: ||| |||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCGTCCCTCAAGAGT 81
          |||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 10
ADD28104
ID   ADD28104 standard; protein; 97 AA.
XX
AC   ADD28104;
XX
DT   15-JAN-2004   (first entry)
XX
DE   Lymphoma related immunoglobulin variable region F5.
XX
KW   B-cell; malignant; immunoglobulin; immunoglobulin variable region;

```
KW   Ig variable region; glycosylation site; lymphoma; B cell receptor;
KW   cytostatic; gene therapy; glycosylation inhibitor;
KW   non-Hodgkin s lymphoma..
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200307409-A2.
XX
PD   12-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-GB000783.
XX
PR   07-MAR-2002; 2002GB-00005395.
XX
PA   (CANC-) CANCER RES TECHNOLOGY LTD.
XX
PI   Zhu D, Stevenson F;
XX
DR   WPI; 2003-902720/82.
XX
PT   Classifying a B-cell as malignant or normal by isolating a sequence
PT   representing an Ig variable region from the B cell, detecting the
PT   presence of a glycosylation site and classifying the cell as malignant or
PT   normal.
XX
PS   Disclosure; Fig 4; 61pp; English.
XX
CC   The present invention describes a method for classifying a B-cell as
CC   malignant or normal comprising: (a) isolating a sequence representing an
CC   immunoglobulin (Ig) variable region from the B cell; and (c) classifying the cell as
CC   presence of a glycosylation site; and (c) classifying the cell as
CC   malignant or normal on the basis of the presence or absence of a
CC   glycosylation site. Also described: (1) treating a patient suffering from
CC   or at risk of having lymphoma; (2) screening for substances capable of
CC   inhibiting glycosylation of the Ig variable region of the B cell receptor
CC   ; and (3) screening for substances (S) capable of inhibiting the
CC   interaction between lectins of the type found in the germinal centre and
CC   N-glycans found on the surface of Ig of lymphoma cells. (S) has
CC   cytostatic activity, and can be used in gene therapy, and as a
CC   glycosylation inhibitor. The method is useful in classifying a B-cell as
CC   malignant or normal. The glycosylation inhibitor is useful in preparing a
CC   medicament for treating non-Hodgkin's lymphoma. The present sequence
CC   represents an Ig variable region sequence which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:             0.000883          Length:        97
Score:                 98.20             Matches:       19
Percent Similarity:    65.62%            Conservative:  2
Best Local Similarity: 59.38%            Mismatches:    3
Query Match:           70.14%            Indels:        8
DB:                    7                 Gaps:          0

NOLAN463-1B.SEQ (1-81) x ADD28104 (1-97)

Qy    2 GGGGGAGTCAGGATATTAGCAGCTGGTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||  ||:::       |||        |||||||||||||||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCCCTCAAGAGT 81
        ||||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 11
ADF10048
ID  ADF10048 standard; protein; 97 AA.
XX
AC  ADF10048;
XX
DT  12-FEB-2004  (first entry)
```

```
XX
DE   VEGF antibody heavy chain variable region VH_4-34.
XX
KW   Antibody; stability; solubility; antigen binding affinity;
KW   variable region; human; VEGF.
XX
OS   Homo sapiens.
XX
PN   WO200307479-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
PS   Example 6; Fig 16a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:             0.000883          Length:        97
Score:                 98.20             Matches:       19
Percent Similarity:    65.62%            Conservative:  2
Best Local Similarity: 59.38%            Mismatches:    3
Query Match:           70.14%            Indels:        8
DB:                    7                 Gaps:          0

NOLAN463-1B.SEQ (1-81) x ADF10048 (1-97)

Qy    2 GGGGGAGTCAGGATATTAGCAGCTGGTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||  ||:::       |||        |||||||||||||||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCCCTCAAGAGT 81
        ||||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 12
ADF10150
ID  ADF10150 standard; protein; 97 AA.
XX
AC  ADF10150;
XX
DT  12-FEB-2004  (first entry)
XX
DE   Antibody heavy chain variable region VH_4-34.
```

Left column:

```
XX
KW   Antibody; stability; solubility; antigen binding affinity;
KW   variable region; human.
XX
OS   Homo sapiens.
XX
PN   WO2003074679-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
PS   Example 16; Fig 40a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.000883            Length:          97
Score:                  98.20               Matches:         19
Percent Similarity:     65.62%              Conservative:    2
Best Local Similarity:  59.38%              Mismatches:      3
Query Match:            70.14%              Indels:          8
DB:                                         Gaps:            0

NOLAN463-1B.SEQ (1-81) x ADF10150 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
                ||| ||:::   ||||||||||||||||||||||||||||||||
Db  42 GlyLys---GlyLeu---GluTrpIleGlyIleAsnHisSerGlySerThrAsnT 59

Qy  62 ACAACCCGTCCCTCAAGAGT 81
                ||||||||||
Db  59 yrAsnProSerLeuLysSer 65

RESULT 13
ADF09942
ID   ADF09942 standard; protein; 97 AA.
XX
AC   ADF09942;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Antibody heavy chain variable region VH_4-34.
XX
KW   Antibody; stability; solubility; antigen binding affinity;
```

Right column:

```
KW   variable region; human.
XX
OS   Homo sapiens.
XX
PN   WO2003074679-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
PS   Disclosure; Fig 2a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The present sequence is an antibody
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.000883            Length:          97
Score:                  98.20               Matches:         19
Percent Similarity:     65.62%              Conservative:    2
Best Local Similarity:  59.38%              Mismatches:      3
Query Match:            70.14%              Indels:          8
DB:                                         Gaps:            0

NOLAN463-1B.SEQ (1-81) x ADF09942 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
                ||| ||:::   ||||||||||||||||||||||||||||||||
Db  42 GlyLys---GlyLeu---GluTrpIleGlyIleAsnHisSerGlySerThrAsnT 59

Qy  62 ACAACCCGTCCCTCAAGAGT 81
                ||||||||||
Db  59 yrAsnProSerLeuLysSer 65

RESULT 14
ADJ80323
ID   ADJ80323 standard; protein; 97 AA.
XX
AC   ADJ80323;
XX
DT   06-MAY-2004 (first entry)
XX
DE   VH gene locus antibody amino acid sequence #43.
XX
KW   hybrid antibody; antibody; framework region; homology; immunogenicity.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200304321-A2.
XX
PD   12-JUN-2003.
XX
PF   03-DEC-2002; 2002WO-US038450.
XX
PR   03-DEC-2001; 2001US-0336591P.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Rother R, Wu D;
XX
DR   WPI; 2003-513753/48.
XX
PT   Producing a hybrid antibody or hybrid antibody fragment by operatively
PT   linking the selected framework sequences to one or more complementarity
PT   determining regions of the initial antibody.
XX
PS   Disclosure; SEQ ID NO 83; 77pp; English.
XX
CC   The invention relates to a method of producing a hybrid antibody or
CC   hybrid antibody fragment by: (i) providing an initial antibody having
CC   specificity for a target; (ii) determining the sequence of a variable
CC   region of the initial antibody; (iii) selecting a first component of the
CC   variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
CC   sequence of the first component to sequencers contained in a reference
CC   database of antibody sequences or antibody fragment sequences from a
CC   target species; (v) selecting a sequence from an antibody in the database
CC   which demonstrates a high degree of homology to the first component; (vi)
CC   selecting a second component of the variable region which is different
CC   than the first component, the second component selected from the group
CC   consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
CC   second component to sequences contained in a reference database of
CC   antibody sequences or antibody fragment sequences from the target species
CC   ; (viii) selecting a sequence from the database which demonstrates a high
CC   degree of homology to the second component and which is from a different
CC   antibody than the selected antibody; and (ix) operatively linking the
CC   selected framework sequences to one or more complementarity determining
CC   regions (CDRs) of the initial antibody to produce a hybrid antibody or
CC   hybrid antibody fragment. The method is useful for producing a hybrid
CC   antibody or hybrid antibody fragment (claimed). The antibody and
CC   fragments are useful for therapeutic and diagnostic purposes. The method
CC   uses entire framework regions from a single antibody variable heavy or
CC   variable light chain to receive the CDRs. This produces antibodies that
CC   are highly homologous and exhibit reduced immunogenicity while
CC   maintaining an optimum binding profile. This sequence represents the
CC   amino acid sequence of an antibody from the VH gene locus.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:           0.000883      Length:              97
Score:               98.20         Matches:             19
Percent Similarity:  65.62%        Conservative:         2
Best Local Similarity: 59.38%      Mismatches:           8
Query Match:         70.14%        Indels:               3
DB:                  7             Gaps:                 0

NOLAN463-1B.SEQ (1-81) x ADJ80323 (1-97)

Qy      2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||::::   ||        |||::| ||||||||||||||||||||||||||
Db     42 GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy     62 ACAACCGTCCCTCAAGAGT 81
          ||||||||||||||||
Db     59 yrAsnProSerLeuLysSer 65
```

RESULT 15
AAB01949

```
ID   AAB01949 standard; protein; 114 AA.
XX
AC   AAB01949;
XX
DT   18-SEP-2000  (first entry)
XX
DE   Anti-Id1 Ab binding-defective mutant Ramos cell VH K70N/S77N.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; heavy chain variable region; VH;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 71
FT                   /note= "Encoded by CAG"
XX
PN   WO200022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999; 99WO-GB003358.
XX
PR   09-OCT-1998; 98GB-00022104.
PR   19-JAN-1999; 99GB-00001141.
PR   09-JUN-1999; 99GB-00013435.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Sale JE, Neuberger MS, Cumbers SJ;
XX
DR   WPI; 2000-317971/27.
DR   N-PSDB; AAA52435.
XX
PT   Lymphoid cell line preparation useful for producing gene products having
PT   desired activity, involves screening and selecting cells having ongoing
PT   target sequence diversification and higher mutation rates.
XX
PS   Example 5; Page; 69pp; English.
XX
CC   The invention relates to a method of preparing a lymphoid cell line
CC   capable of capable of directed constitutive hypermutation of a target
CC   nucleic acid region. The method comprises screening a cell population for
CC   ongoing target sequence diversification and selecting a cell in which the
CC   rate of target nucleic acid mutation exceeds that of other nucleic acid
CC   mutation by a factor of 100 or more. The invention also relates to a
CC   method for preparing a gene product with a desired activity, comprising
CC   expressing a nucleic acid encoding the target gene operably linked to a
CC   sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC   transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC   cells which express a mutated gene product with the desired activity. One
CC   or more clonal populations of the identified cells is established, and
CC   cells with an improved activity of interest are selected. These steps may
CC   be iteratively repeated until a gene product with a desired of activity
CC   is obtained. The cell lines prepared according to the method of the
CC   invention are used for directed constitutive hypermutation of a nucleic
CC   acid region in the preparation of a gene product, preferably an enzyme or
CC   an immunoglobulin (Ig) with a desired activity. In the exemplifications
CC   of the invention, IgM-secreting Ramos cells were selected for use as they
CC   undergo hypermutation during clonal expansion. This was determined on the
CC   basis of the amount of diversity in the heavy chain variable region (VH).
CC   Sequences AAB01949-B01954 represent various mutant Ramos cell IgM VHs
CC   (AAB01949-B01954) which have lost the ability to bind anti-idiotype
CC   antibodies (anti-Id1 Ab) relative to the wild-type VH (AAB01948). Note:
CC   The present sequence is not shown in the specification, but is derived
CC   from the wild-type Ramos cell VH shown in figure 7
XX
SQ   Sequence 114 AA;

Alignment Scores:
Pred. No.:           0.00092       Length:              114
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Score:                 98.20       Matches:        19
Percent Similarity:    65.62%      Conservative:    2
Best Local Similarity: 59.38%      Mismatches:      3
Query Match:           70.14%      Indels:          8
DB:                    3           Gaps:            0
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NOLAN463-1B.SEQ (1-81) x AAB01949 (1-114)

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Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
        |||:::    |||     |||:::   |||||||||||||||||||||||||||||||
Db   36 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 53

Qy   62 ACAACCCGTCCCTCAAGAGT 81
        |||||||||||||||||||
Db   53 yrAsnProSerLeuLysSer 59
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Search completed: August 4, 2005, 18:14:25
Job time : 93.5 secs

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                 GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:   August  4, 2005, 18:05:28 ; Search time 23.25 seconds
                                        (without alignments)
                                        520.135 Million cell updates/sec

Title:         NOLAN463-1B.SEQ
Perfect score: 140
Sequence:      1 CGGGCGAGTCAGGATATTAG.........ACAACCGTCCTCAAGAGT 81

Scoring table: BLOSUM62
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               Ygapop 10.0 , Ygapext  0.1
               Fgapop  6.0 , Fgapext  0.1
               Delop   6.0 , Delext   0.1

Searched:      513545 seqs, 7464906+ residues

Total number of hits satisfying chosen parameters:     1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-1/runat_04082005_125807_24557//app_query.fasta_1.5
-DB=Issued_Patents_AA -QFMT=fastan -SUFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN_1_1 66 @runat_04082005_125807_24557 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :     Issued_Patents AA:*
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          2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
          3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
          4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
          5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	98.2	70.1	116	3	US-08-545-809A-118	Sequence 118, App
2	98.2	70.1	123	4	US-08-793-450-4	Sequence 4, Appli
3	98.2	70.1	139	4	US-09-203-768A-2	Sequence 2, Appli
4	98.2	70.1	472	3	US-08-793-450-8	Sequence 8, Appli
5	93.2	66.6	429	4	US-09-372-425A-6	Sequence 6, Appli
6	92.1	65.8	118	3	US-09-025-769B-25	Sequence 25, Appl
7	92.1	65.8	118	4	US-09-490-070A-25	Sequence 25, Appl
8	92.1	65.8	118	4	US-09-490-153-25	Sequence 25, Appl
9	92.1	65.8	118	4	US-09-490-324-25	Sequence 25, Appl
10	91.1	65.1	120	3	US-08-545-809A-137	Sequence 137, App
11	87.2	62.3	147	4	US-09-471-276-835	Sequence 835, App
12	86.3	61.6	130	3	US-08-466-151-5	Sequence 5, Appli
13	86.3	61.6	130	3	US-08-466-163B-5	Sequence 5, Appli
14	86.3	61.6	130	4	US-09-802-095-5	Sequence 5, Appli
15	86.3	61.6	130	4	US-09-802-077-5	Sequence 5, Appli
16	85.2	60.9	447	4	US-09-372-425A-2	Sequence 2, Appli
17	83.1	59.4	118	2	US-08-552-816A-13	Sequence 13, App
18	83.1	59.4	139	4	US-09-471-276-837	Sequence 837, App
19	83.1	59.4	244	3	US-08-918-148-79	Sequence 79, Appl
20	81.2	58.0	244	4	US-09-138-091A-77	Sequence 77, Appl
21	81.2	58.0	119	2	US-08-428-197-16	Sequence 16, Appl
22	81.2	58.0	119	5	PCT-US93-10555-16	Sequence 16, Appl
23	80.1	57.2	100	4	US-09-726-219A-169	Sequence 169, App
24	80.1	57.2	117	4	US-09-720-493-2	Sequence 2, Appli
25	79.3	56.6	100	2	US-08-273-146-69	Sequence 69, Appl
26	79.3	56.6	137	3	US-08-466-151-7	Sequence 7, Appli
27	79.3	56.6	137	4	US-08-466-163B-7	Sequence 7, Appli
28	79.3	56.6	137	4	US-09-802-096-7	Sequence 7, Appli
29	79.3	56.6	137	4	US-09-802-077-7	Sequence 7, Appli
30	79.1	56.5	119	3	US-09-025-769B-39	Sequence 39, Appl
31	79.1	56.5	119	3	US-09-025-769B-65	Sequence 65, Appl
32	79.1	56.5	119	4	US-09-490-070A-39	Sequence 39, Appl
33	79.1	56.5	119	4	US-09-490-070A-65	Sequence 65, Appl
34	79.1	56.5	119	4	US-09-490-153-39	Sequence 39, Appl
35	79.1	56.5	119	4	US-09-490-153-65	Sequence 65, Appl
36	79.1	56.5	119	4	US-09-490-324-39	Sequence 39, Appl
37	79.1	56.5	119	4	US-09-490-324-65	Sequence 65, Appl
38	78.3	55.9	118	4	US-09-343-698-6	Sequence 6, Appli
39	78.3	55.9	118	4	US-08-325-955-6	Sequence 6, Appli
40	78.3	55.9	119	3	US-08-767-128-18	Sequence 18, Appl
41	78.3	55.9	213	4	US-09-170-769A-2	Sequence 2, Appli
42	78.3	55.9	832	4	US-08-630-820-7	Sequence 7, Appli
43	78.3	55.9	832	4	US-09-273-453-7	Sequence 7, Appli
44	78.1	55.8	116	3	US-08-545-809A-140	Sequence 140, App
45	77.9	55.6	76	3	US-08-851-362D-22	Sequence 22, Appl

ALIGNMENTS

```
RESULT 1
US-08-545-809A-118

; Sequence 118, Application US/0854580+9A
; Patent No. 6096878
; GENERAL INFORMATION:
;  APPLICANT: Honjo, Tasuku
;  APPLICANT: Matsuda, Fumihiko
;  TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;  TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;  NUMBER OF SEQUENCES: 145
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Fish & Richardson, P.C.
;  STREET: 225 Franklin Street
;  CITY: Boston
;  STATE: MA
;  COUNTRY: US
;  ZIP: 02110-2804
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette
;  COMPUTER: IBM Compatible
;  OPERATING SYSTEM: Windows95
;  SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/545,809A
;  FILING DATE: 27-MAR-1996
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: PCT/JP93/00603
;  FILING DATE: 10-MAY-1993
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Freeman, John W.
;  REGISTRATION NUMBER: 29,066
;  REFERENCE/DOCKET NUMBER: 06501/004001
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 617-542-5070
;  TELEFAX: 617-542-8906
;  TELEX: 200154
```

```
;  INFORMATION FOR SEQ ID NO: 118:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 116 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-545-809A-118
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Alignment Scores:
Pred. No.:                7.72e-05      Length:            116
Score:                    98.20         Matches:           19
Percent Similarity:       65.62%        Conservative:      2
Best Local Similarity:    59.38%        Mismatches:        3
Query Match:              70.14%        Indels:            8
DB:                       3             Gaps:              0
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NOLAN463-1B.SEQ (1-81) x US-08-545-809A-118 (1-116)

Qy      2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||| ::::  ||      ||  :::   |||||||||||||||||||||||||||||||
Db     61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78

Qy     62 ACAACCCGTCCCTCAAGAGT 81
          ||||||||||||||||||||
Db     78 yrAsnProSerLeuLysSer 84
```

```
RESULT 2
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
;  GENERAL INFORMATION:
;    APPLICANT: EDELMAN, LENA
;    APPLICANT: MARGARITTE, CHRISTEL
;    APPLICANT: KACZOREK, MICHEL
;    APPLICANT: CHAABIHI, HASSAN
;  TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;  TITLE OF INVENTION:
;  NUMBER OF SEQUENCES: 25
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;    ADDRESSEE: P.C.
;    STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;    CITY: ARLINGTON
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22202
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/793,450
;    FILING DATE: 03-MAR-1997
;    CLASSIFICATION: 536
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: FR 94/10566
;    FILING DATE: 02-SEP-1994
;  ATTORNEY/AGENT INFORMATION:
;    NAME: OBLON, NORMAN F.
;    REGISTRATION NUMBER: 24,618
;    REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-413-3000
;    TELEFAX: 703-413-2220
;  INFORMATION FOR SEQ ID NO: 4:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 123 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-793-450-4
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Alignment Scores:
Pred. No.:                7.89e-05      Length:            123
Score:                    98.20         Matches:           19
Percent Similarity:       65.62%        Conservative:      2
Best Local Similarity:    59.38%        Mismatches:        3
Query Match:              70.14%        Indels:            8
DB:                       3             Gaps:              0
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NOLAN463-1B.SEQ (1-81) x US-08-793-450-4 (1-123)

Qy      2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||| ::::  ||      ||  :::   |||||||||||||||||||||||||||||||
Db     42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 65

Qy     62 ACAACCCGTCCCTCAAGAGT 81
          ||||||||||||||||||||
Db     59 yrAsnProSerLeuLysSer 65
```

```
RESULT 3
US-09-203-768A-2
; Sequence 2, Application US/09203768A
; Patent No. 6787638
;  GENERAL INFORMATION:
;    APPLICANT: Huse, William D.
;    APPLICANT: Watkins, Jeffry D.
;  TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
;  TITLE OF INVENTION: of Use
;  FILE REFERENCE: P-IX 2947
;  CURRENT APPLICATION NUMBER: US/09/203,768A
;  CURRENT FILING DATE: 1998-12-02
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 139
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-203-768A-2
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```
Alignment Scores:
Pred. No.:                8.25e-05      Length:            139
Score:                    98.20         Matches:           19
Percent Similarity:       65.62%        Conservative:      2
Best Local Similarity:    59.38%        Mismatches:        3
Query Match:              70.14%        Indels:            8
DB:                       4             Gaps:              0
```

```
NOLAN463-1B.SEQ (1-81) x US-09-203-768A-2 (1-139)

Qy      2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||| ::::  ||      ||  :::   |||||||||||||||||||||||||||||||
Db     61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78

Qy     62 ACAACCCGTCCCTCAAGAGT 81
          ||||||||||||||||||||
Db     78 yrAsnProSerLeuLysSer 84
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```
RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
;  GENERAL INFORMATION:
;    APPLICANT: EDELMAN, LENA
;    APPLICANT: MARGARITTE, CHRISTEL
;    APPLICANT: KACZOREK, MICHEL
;    APPLICANT: CHAABIHI, HASSAN
;  TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;  TITLE OF INVENTION:
;  NUMBER OF SEQUENCES: 25
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;    ADDRESSEE: P.C.
;    STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;    CITY: ARLINGTON
```

```
;         STATE: VA
;         COUNTRY: USA
;         ZIP: 22202
;     COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/08/793,450
;         FILING DATE: 03-MAR-1997
;         CLASSIFICATION: 536
;     PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: FR 94/10566
;         FILING DATE: 02-SEP-1994
;     ATTORNEY/AGENT INFORMATION:
;         NAME: OBLON, NORMAN F.
;         REGISTRATION NUMBER: 24,618
;         REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;     TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 703-413-3000
;         TELEFAX: 703-413-2220
;     INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 472 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-793-450-8

Alignment Scores:
Pred. No.:                0.00013          Length:          472
Score:                    98.20            Matches:         19
Percent Similarity:       65.62%           Conservative:    2
Best Local Similarity:    59.38%           Mismatches:      3
Query Match:              70.14%           Indels:          8
DB:                                        Gaps:            0

NOLAN463-1B.SEQ (1-81) x US-08-793-450-8 (1-472)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          |||::|   ||   |||:::  |||||||||||||||||||||
Db   61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  78

Qy   62 ACAACCCGTCCTCAAGAGT 81
          |||||||||||||||
Db   78 yrAsnProSerLeuLysSer 84

RESULT 5
US-09-372-425A-6
; Sequence 6, Application US/09372425A
; Patent No. 6475749
;   GENERAL INFORMATION:
;     APPLICANT: Sherie L. Morrison
;     APPLICANT: Ramon Montano
;     TITLE OF INVENTION: Improved Rh Antibody
;     NUMBER OF SEQUENCES: 11
;     CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
;         STREET: 2029 Century Park East, Suite 3800
;         CITY: Los Angeles
;         STATE: CA
;         COUNTRY: USA
;         ZIP: 90067
;     COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy Disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: Windows 98
;         SOFTWARE: MS Word
;     CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/372,425A
;         FILING DATE: August 11, 1999
;         CLASSIFICATION: 435
```

```
;     PRIOR APPLICATION DATA:
;         APPLICATION NUMBER:
;         FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;         NAME: Oldenakmp, David J.
;         REGISTRATION NUMBER: 29,421
;         REFERENCE/DOCKET NUMBER: 510015-223
;     TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (310) 788-5000
;         TELEFAX: (310) 788-5100
;     INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 429 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;     MOLECULE TYPE: Heavy chain without Tailpiece - AA
US-09-372-425A-6

Alignment Scores:
Pred. No.:                0.000592         Length:          429
Score:                    93.20            Matches:         18
Percent Similarity:       65.62%           Conservative:    3
Best Local Similarity:    56.25%           Mismatches:      3
Query Match:              66.57%           Indels:          8
DB:                                        Gaps:            0

NOLAN463-1B.SEQ (1-81) x US-09-372-425A-6 (1-429)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          |||::|   ||   |||:::  |||||||||||||||||:|||
Db   61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAspHisSerGlySerThrAsnT  78

Qy   62 ACAACCCGTCCTCAAGAGT 81
          |||||||||||||||
Db   78 yrAsnProSerLeuLysSer 84

RESULT 6
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 6300064
;   GENERAL INFORMATION:
;     APPLICANT: Knappik, Achim
;     APPLICANT: Pack, Peter
;     APPLICANT: Ilag, Vic
;     APPLICANT: Ge, Liming
;     APPLICANT: Moroney, Simon
;     APPLICANT: Plueckthun, Andreas
;     TITLE OF INVENTION: Protein/(Poly)peptide libraries
;     NUMBER OF SEQUENCES: 373
;     CORRESPONDENCE ADDRESS:
;         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;         STREET: 1251 Avenue of the Americas
;         CITY: New York
;         STATE: New York
;         COUNTRY: USA
;         ZIP: 10021
;     COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/025,769B
;         FILING DATE: 18-FEB-1998
;     PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: EP 95 11 3021.0
;         FILING DATE: 18-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;         NAME: James F. Haley, Jr., Esq.
;         REGISTRATION NUMBER: 27,794
;         REFERENCE/DOCKET NUMBER: MORPHO/5
;     TELECOMMUNICATION INFORMATION:
```

```
             TELEPHONE:  (212)596-9000
             TELEFAX:    (212)596-9090
;     INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 118 amino acids
;         TYPE: amino acid
;         STRANDEDNESS:
;         TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-09-025-769B-25

Alignment Scores:
Pred. No.:              0.000517      Length:         118
Score:                  92.10         Matches:         21
Percent Similarity:     50.00%        Conservative:     1
Best Local Similarity:  47.73%        Mismatches:       3
Query Match:            65.79%        Indels:          19
DB:                                   Gaps:             1

NOLAN463-1B.SEQ (1-81) x US-09-025-769B-25 (1-118)

Qy    3 GGCGAGTCAGGATATTAGCAGC------------------------------    24
         |||  |||    ||||||
Db   26 GlyGlySer----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl   44

Qy   25 -----TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA   77
             |||::| |||||||||||||||||||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy   77

Qy   78 GAGT   81
         |||
Db   64 sSer   65

RESULT 7
US-09-490-070A-25
;  Sequence 25, Application US/09490070A
;  Patent No. 6696248
;  GENERAL INFORMATION:
      APPLICANT: Knappik, Achim
                 Pack, Peter
                 Ilag, Vic
                 Ge, Liming
                 Moroney, Simon
                 Plueckthun, Andreas
      TITLE OF INVENTION: Protein/(Poly)peptide libraries
      NUMBER OF SEQUENCES: 373
      CORRESPONDENCE ADDRESS:
         ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
                    White & McAuliffe
         STREET: 1666 K Street, N.W., Suite 300
         CITY: Washington
         STATE: D.C.
         COUNTRY: USA
         ZIP: 20006
      COMPUTER READABLE FORM:
         MEDIUM TYPE: Floppy disk
         COMPUTER: IBM PC compatible
         OPERATING SYSTEM: PC-DOS/MS-DOS
         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
      CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/09/490,070A
         FILING DATE: 24-Jan-2000
      PRIOR APPLICATION DATA:
         APPLICATION NUMBER: EP 95 11 3021.0
         FILING DATE: 18-AUG-1995
      ATTORNEY/AGENT INFORMATION:
         NAME: Colin G. Sandercock, Esq.
         REGISTRATION NUMBER: 31,298
         REFERENCE/DOCKET NUMBER: 37629-0005
      TELECOMMUNICATION INFORMATION:
         TELEPHONE: (202) 912-2000
         TELEFAX: (202) 912-2020
;     INFORMATION FOR SEQ ID NO: 25:
```

```
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 118 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: <Unknown>
;         TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Alignment Scores:
Pred. No.:              0.000517      Length:         118
Score:                  92.10         Matches:         21
Percent Similarity:     50.00%        Conservative:     1
Best Local Similarity:  47.73%        Mismatches:       3
Query Match:            65.79%        Indels:          19
DB:                                   Gaps:             1

NOLAN463-1B.SEQ (1-81) x US-09-490-070A-25 (1-118)

Qy    3 GGCGAGTCAGGATATTAGCAGC------------------------------    24
         |||  |||    ||||||
Db   26 GlyGlySer----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl   44

Qy   25 -----TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA   77
              ||::| |||||||||||||||||||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy   64

Qy   78 GAGT   81
         |||
Db   64 sSer   65

RESULT 8
US-09-490-153-25
;  Sequence 25, Application US/09490153
;  Patent No. 6706484
;  GENERAL INFORMATION:
      APPLICANT: Knappik, Achim
                 Pack, Peter
                 Ilag, Vic
                 Ge, Liming
                 Moroney, Simon
                 Plueckthun, Andreas
      TITLE OF INVENTION: Protein/(Poly)peptide libraries
      NUMBER OF SEQUENCES: 373
      CORRESPONDENCE ADDRESS:
         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
         STREET: 1251 Avenue of the Americas
         CITY: New York
         STATE: New York
         COUNTRY: USA
         ZIP: 10021
      COMPUTER READABLE FORM:
         MEDIUM TYPE: Floppy disk
         COMPUTER: IBM PC compatible
         OPERATING SYSTEM: PC-DOS/MS-DOS
         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
      CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/09/490,153
         FILING DATE: 24-Jan-2000
      PRIOR APPLICATION DATA:
         APPLICATION NUMBER: US/09/025,769B
         FILING DATE: 18-FEB-1998
         APPLICATION NUMBER: EP 95 11 3021.0
         FILING DATE: 18-AUG-1995
      ATTORNEY/AGENT INFORMATION:
         NAME: James F. Haley, Jr., Esq.
         REGISTRATION NUMBER: 27,794
         REFERENCE/DOCKET NUMBER: MORPHO/5
      TELECOMMUNICATION INFORMATION:
         TELEPHONE: (212)596-9000
         TELEFAX: (212)596-9090
;     INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
```

LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Alignment Scores:
Pred. No.:   0.000517   Length: 118
Score: 92.10   Matches: 21
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.73%   Mismatches: 3
Query Match: 65.79%   Indels: 19
DB: Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-490-153-25 (1-118)

Qy   3 GGCGAGTCAGGATATTAGCAGC------------------------ 24
          ||| ||| ||||||||||
Db   26 GlyGlySer-----IleSerSerTyrTyrSerTrpTrpIleArgGlnProProGlyLysGl 44

Qy   25 ------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAA 77
               |||:: ||||| |||||||||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
          |||
Db   64 sSer 65

RESULT 9
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
APPLICANT: Knappik, Achim
           Pack, Peter
           Ilag, Vic
           Ge, Liming
           Moroney, Simon
           Plueckthun, Andreas
TITLE OF INVENTION: Protein-/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids

TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Alignment Scores:
Pred. No.:   0.000517   Length: 118
Score: 92.10   Matches: 21
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.73%   Mismatches: 3
Query Match: 65.79%   Indels: 19
DB: Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-490-324-25 (1-118)

Qy   3 GGCGAGTCAGGATATTAGCAGC------------------------ 24
          ||| ||| ||||||||||
Db   26 GlyGlySer-----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl 44

Qy   25 ------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAA 77
               |||:: ||||| |||||||||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
          |||
Db   64 sSer 65

RESULT 10
US-08-545-809A-137
; Sequence 137, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-137

```
Alignment Scores:
Pred. No.:                 0.00071        Length:          120
Score:                     91.10          Matches:          20
Percent Similarity:        52.27%         Conservative:      3
Best Local Similarity:     45.45%         Mismatches:        2
Query Match:               65.07%         Indels:           19
DB:                                       Gaps:              1

NOLAN463-1B.SEQ (1-81) x US-08-545-809A-137 (1-120)

Qy   3 GGCGAGTCAGGATATTAGCAGC------------------------ 24
         |||:::||| ||||||||
Db  45 GlyAspSer----IleSerGlyAsnTrpIleTrpValArgGlnProGlyLysGl 63

Qy  25 -------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACCCGTCCCTCAA 77
               ||||||||||||||||||||
Db  63 yLeuGluTrpIleGlyGluIleHisHisSerGlySerThrThrTyrTyrAsnProSerLeuLyY 83

Qy  78 GAGT 81
        |||
Db  83 sSer 84

RESULT 11
US-09-471-276-835
; Sequence 835, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 835
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -26..-1
US-09-471-276-835

Alignment Scores:
Pred. No.:                 0.00257        Length:          147
Score:                     87.20          Matches:          16
Percent Similarity:        65.62%         Conservative:      5
Best Local Similarity:     50.00%         Mismatches:        3
Query Match:               62.29%         Indels:            8
DB:                                       Gaps:              0

NOLAN463-1B.SEQ (1-81) x US-09-471-276-835 (1-147)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         |||:::|| ||| ||:::||| ||:::||||||
Db  69 GlyLys----GlyLeu---GluTrpIleSerGluIleAspHisGlyGlyAsnThrAsnT 86

Qy  62 ACAACCCGTCCCTCAAGAGT 81
        ||||||||||||||
Db  86 yrAsnProSerLeuLysSer 92

RESULT 12
US-08-466-151-5
; Sequence 5, Application US/08466151
```

```
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9981
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.:                 0.00325        Length:          130
Score:                     86.30          Matches:          17
Percent Similarity:        40.74%         Conservative:      5
Best Local Similarity:     31.48%         Mismatches:        5
Query Match:               61.64%         Indels:           27
DB:                                       Gaps:              1

NOLAN463-1B.SEQ (1-81) x US-08-466-151-5 (1-130)

Qy   1 CGGGCGAGTCAGGATATTAGC------------------------------------------ 21
         ::: ||||| ::||||
Db  13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32

Qy  22 -------------------------------------AGCTGGTGGTTAGCCGAAATC 39
                                              |||:::
Db  33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy  40 AATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT 81
        ||||||||||||||||||||||||||
Db  53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 13
```

US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.:   0.00325   Length: 130
Score: 86.30   Matches: 17
Percent Similarity: 40.74%   Conservative: 5
Best Local Similarity: 31.48%   Mismatches: 5
Query Match: 61.64%   Indels: 27
DB: 3   Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-08-466-163B-5 (1-130)

Qy   1 CGGGCGAGTCAGGATATTAGC-------------------------------- 21
               ::: |||||| ::||||
Db 13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32

Qy 22 --AGCTGGTTAGCCGAAATC 39
                                              |||:::
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy 40 AATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT 81
        ||||||||||||:::||::||||:::||||||||||||||||
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 14
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-5

Alignment Scores:
Pred. No.:   0.00325   Length: 130
Score: 86.30   Matches: 17
Percent Similarity: 40.74%   Conservative: 5
Best Local Similarity: 31.48%   Mismatches: 5
Query Match: 61.64%   Indels: 27
DB: 4   Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-802-096-5 (1-130)

Qy   1 CGGGCGAGTCAGGATATTAGC-------------------------------- 21
               ::: |||||| ::||||
Db 13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32

Qy 22 --AGCTGGTTAGCCGAAATC 39
                                              |||:::
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy 40 AATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT 81
        ||||||||||||:::||::||||:::||||||||||||||||
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 15
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Alignment Scores:
Pred. No.:   0.00325   Length: 130
Score: 86.30   Matches: 17
Percent Similarity: 40.74%   Conservative: 5
Best Local Similarity: 31.48%   Mismatches: 5
Query Match: 61.64%   Indels: 27
DB: 4   Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-802-077-5 (1-130)

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Qy 22 --AGCTGGTTAGCCGAAATC 39
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Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy 40 AATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGT 81
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Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

nolan463-1b.seq.rai

Fri Aug 5 09:28:03 2005

Search completed: August 4, 2005, 18:23:04
Job time : 24.25 secs

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	100.1	71.5	253	10	US-09-880-748-1333	Sequence 1333, Ap
2	100.1	71.5	253	15	US-10-293-418-1333	Sequence 1333, Ap
3	99.9	71.4	125	15	US-10-371-942-118	Sequence 118, App
4	98.2	70.1	80	14	US-10-078-958-2	Sequence 2, Appli
5	98.2	70.1	97	14	US-10-194-975-40	Sequence 40, Appl
6	98.2	70.1	97	15	US-10-308-817-83	Sequence 83, Appl
7	98.2	70.1	97	15	US-10-032-037B-87	Sequence 87, Appl
8	98.2	70.1	97	15	US-10-029-988B-87	Sequence 87, Appl
9	98.2	70.1	97	15	US-10-032-423A-87	Sequence 87, Appl
10	98.2	70.1	97	15	US-10-455-698-83	Sequence 83, Appl
11	98.2	70.1	97	15	US-10-029-926B-87	Sequence 87, Appl
12	98.2	70.1	97	16	US-10-379-392-47	Sequence 47, Appl
13	98.2	70.1	114	17	US-10-733-532-128	Sequence 128, App
14	98.2	70.1	115	17	US-10-898-408-12	Sequence 12, Appl
15	98.2	70.1	117	9	US-09-864-761-44315	Sequence 44315, A
16	98.2	70.1	118	15	US-10-371-942-90	Sequence 90, Appl
17	98.2	70.1	118	17	US-10-893-576-192	Sequence 192, App
18	98.2	70.1	122	15	US-10-360-828-63	Sequence 63, Appl
19	98.2	70.1	125	15	US-10-371-942-110	Sequence 110, App
20	98.2	70.1	139	14	US-10-300-675-2	Sequence 2, Appli
21	98.2	70.1	139	17	US-10-910-124-2	Sequence 2, Appli
22	98.2	70.1	139	17	US-10-895-576-43	Sequence 43, Appl
23	98.2	70.1	142	17	US-10-484-790A-10	Sequence 10, Appl
24	98.2	70.1	223	10	US-09-972-656-66	Sequence 66, Appl
25	98.2	70.1	229	10	US-09-972-656-82	Sequence 82, Appl
26	98.2	70.1	230	10	US-09-972-656-72	Sequence 72, Appl
27	98.2	70.1	249	10	US-09-880-748-1321	Sequence 1321, Ap
28	98.2	70.1	249	15	US-10-293-418-1321	Sequence 1321, Ap
29	98.2	70.1	250	10	US-09-880-748-1413	Sequence 1413, Ap
30	98.2	70.1	250	15	US-10-293-418-1413	Sequence 1413, Ap
31	98.2	70.1	254	10	US-09-880-748-1659	Sequence 1659, Ap
32	98.2	70.1	254	15	US-10-293-418-1659	Sequence 1659, Ap
33	98.2	70.1	450	17	US-10-484-790A-17	Sequence 17, Appl
34	98.2	70.1	453	17	US-10-484-790A-18	Sequence 18, Appl
35	97.2	69.4	249	10	US-09-880-748-957	Sequence 957, App
36	97.2	69.4	249	15	US-10-293-418-957	Sequence 957, App
37	95	67.9	246	10	US-09-880-748-1847	Sequence 1847, Ap
38	95	67.9	246	15	US-10-293-418-1847	Sequence 1847, Ap
39	94.2	67.3	123	14	US-10-269-805-31	Sequence 31, Appl
40	94.2	67.3	123	14	US-10-269-805-55	Sequence 55, Appl
41	94.2	67.3	255	10	US-09-880-748-1642	Sequence 1642, Ap
42	94.2	67.3	255	15	US-10-293-418-1642	Sequence 1642, Ap
43	93.7	66.9	116	15	US-10-308-817-189	Sequence 189, App
44	93.7	66.9	116	15	US-10-453-698-189	Sequence 189, App
45	93.2	66.6	250	10	US-09-880-748-993	Sequence 993, App

ALIGNMENTS

RESULT 1
US-09-880-748-1333
; Sequence 1333, Application US/09880748
; Publication No. US2003059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

OM nucleic - protein search, using frame_plus_n2p model

    Copyright   GenCore version 5.1.6
    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 4, 2005, 18:20:25 ; Search time 80.25 Seconds
                                       (without alignments)
                                788.093 Million cell updates/sec

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Perfect score: 140
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    Ygapop 10.0 , Ygapext   0.1
    Fgapop   6.0 , Fgapext   0.1
    Delop   6.0 , Delext   0.1

Searched: 1752860 seqs, 39039742 residues

Total number of hits satisfying chosen parameters: 3505720

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :   Published Applications AA:*
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   21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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;   PRIOR FILING DATE: 2001-05-25
;   NUMBER OF SEQ ID NOS: 3239
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1333

Alignment Scores:
Pred. No.:              0.00155
Score:                  100.10
Percent Similarity:     50.00%
Best Local Similarity:  47.73%
Query Match:            71.50%
DB:                     10

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Qy       18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACCCGTCCCTCAA 77
            |||::: ||||||||||||||||||||||||||||||||||||||||||||||
Db       46 ---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy       78 GAGT 81
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Db       64 sSer 65

RESULT 2
US-10-293-418-1333
;   Sequence 1333, Application US/10293418
;   Publication No. US20030223996A1
;   GENERAL INFORMATION:
;     APPLICANT: Ruben et al.
;     TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;     FILE REFERENCE: PF523P2
;     CURRENT APPLICATION NUMBER: US/10/293,418
;     CURRENT FILING DATE: 2002-11-27
;     PRIOR APPLICATION NUMBER: 60/331,469
;     PRIOR FILING DATE: 2001-11-16
;     PRIOR APPLICATION NUMBER: 60/340,817
;     PRIOR FILING DATE: 2001-12-19
;     PRIOR APPLICATION NUMBER: 09/880,748
;     PRIOR FILING DATE: 2001-06-15
;     PRIOR APPLICATION NUMBER: 60/293,499
;     PRIOR FILING DATE: 2001-05-25
;     PRIOR APPLICATION NUMBER: 60/277,379
;     PRIOR FILING DATE: 2001-03-21
;     PRIOR APPLICATION NUMBER: 60/276,248
;     PRIOR FILING DATE: 2001-03-16
;     PRIOR APPLICATION NUMBER: 60/240,816
;     PRIOR FILING DATE: 2000-10-17
;     PRIOR APPLICATION NUMBER: 60/212,210
;     PRIOR FILING DATE: 2000-06-16
;   NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1333
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-1333

Alignment Scores:
Pred. No.:              0.00155
Score:                  100.10
Percent Similarity:     50.00%
Best Local Similarity:  47.73%
Query Match:            71.50%
DB:                     15

NOLAN463-1B.SEQ (1-81) x US-10-293-418-1333 (1-253)
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Qy        3 GGCGAGTCA 17
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Db       26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy       18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACCCGTCCCTCAA 77
            |||::: ||||||||||||||||||||||||||||||||||||||||||||||
Db       46 ---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy       78 GAGT 81
            ||||
Db       64 sSer 65

RESULT 3
US-10-371-942-118
;   Sequence 118, Application US/10371942
;   Publication No. US20030223994A1
;   GENERAL INFORMATION:
;     APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
;     APPLICANT: Reiter, Yoram
;     TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
;     FILE REFERENCE: 10280-034001
;     CURRENT APPLICATION NUMBER: US/10/371,942
;     CURRENT FILING DATE: 2003-02-20
;     PRIOR APPLICATION NUMBER: US 60/358,994
;     PRIOR FILING DATE: 2002-02-20
;   NUMBER OF SEQ ID NOS: 121
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 118
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-371-942-118

Alignment Scores:
Pred. No.:              0.00146
Score:                  99.90
Percent Similarity:     50.00%
Best Local Similarity:  47.83%
Query Match:            71.36%
DB:                     15

NOLAN463-1B.SEQ (1-81) x US-10-371-942-118 (1-125)

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Db       26 GlyGlySer----IleSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44

Qy       25 -----TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACCCGTC 71
            |||::|||GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64
Db       44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64

Qy       72 CCTCAAGAGT 81
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Db       64 rLeuLysSer 67

RESULT 4
US-10-078-958-2
;   Sequence 2, Application US/10078958
;   Publication No. US20030070185A1
;   GENERAL INFORMATION:
;     APPLICANT: JAKOBOVITS, AYA
;     APPLICANT: KUCHERLAPATI, RAJU
;     APPLICANT: KLAPHOLZ, SUSAN
;     APPLICANT: MENDEZ, MICHAEL J.
;     APPLICANT: GREEN, LARRY
;     TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;     TITLE OF INVENTION: PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;     TITLE OF INVENTION: THEREFROM
;     FILE REFERENCE: CELL 4.18 CON
;     CURRENT APPLICATION NUMBER: US/10/078,958
;     CURRENT FILING DATE: 2002-02-19
;     PRIOR APPLICATION NUMBER: 08/759,620
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;   PRIOR FILING DATE: 1996-12-03
;   NUMBER OF SEQ ID NOS: 79
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 2
;     LENGTH: 80
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-10-078-958-2

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Best Local Similarity:              59.38%         Mismatches:       3
Query Match:                        70.14%         Indels:           8
DB:                                 14             Gaps:             0

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Qy     62 ACAACCCGTCCCTCAAGAGT 81
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Db     42 yrAsnProSerLeuLysSer 48

RESULT 5
US-10-194-975-40
;   Sequence 40, Application US/10194975
;   Publication No. US2003003649A1
;   GENERAL INFORMATION:
;   APPLICANT: Foote, Jefferson
;   TITLE OF INVENTION: Super Humanized Antibodies
;   FILE REFERENCE: 501231.01
;   CURRENT APPLICATION NUMBER: US/10/194,975
;   CURRENT FILING DATE: 2002-10-10
;   PRIOR APPLICATION NUMBER: US 60/305,111
;   PRIOR FILING DATE: 2001-07-12
;   NUMBER OF SEQ ID NOS: 122
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 40
;     LENGTH: 97
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-10-194-975-40

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Pred. No.:                          0.00228        Length:           97
Score:                              98.20          Matches:          19
Percent Similarity:                 65.62%         Conservative:     2
Best Local Similarity:              59.38%         Mismatches:       3
Query Match:                        70.14%         Indels:           8
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Db     42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy     62 ACAACCCGTCCCTCAAGAGT 81
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Db     59 yrAsnProSerLeuLysSer 65

RESULT 6
US-10-308-817-83
;   Sequence 83, Application US/10308817
;   Publication No. US2003021986lA1
;   GENERAL INFORMATION:
;   APPLICANT: Rother, Russell
;   APPLICANT: Wu, Dayang
;   TITLE OF INVENTION: HYBRID ANTIBODIES
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;   FILE REFERENCE: 1087-37
;   CURRENT APPLICATION NUMBER: US/10/308,817
;   CURRENT FILING DATE: 2002-12-03
;   NUMBER OF SEQ ID NOS: 195
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 83
;     LENGTH: 97
;     TYPE: PRT
;     ORGANISM: human
US-10-308-817-83

Alignment Scores:
Pred. No.:                          0.00228        Length:           97
Score:                              98.20          Matches:          19
Percent Similarity:                 65.62%         Conservative:     2
Best Local Similarity:              59.38%         Mismatches:       3
Query Match:                        70.14%         Indels:           8
DB:                                 15             Gaps:             0

NOLAN463-1B.SEQ (1-81) x US-10-308-817-83 (1-97)

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Db     42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy     62 ACAACCCGTCCCTCAAGAGT 81
          ||||||||||||||||||||
Db     59 yrAsnProSerLeuLysSer 65

RESULT 7
US-10-032-037B-87
;   Sequence 87, Application US/10032037B
;   Publication No. US2004001822A1
;   GENERAL INFORMATION:
;   APPLICANT: Bio-Technology General Corp.
;   TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
;   TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
;   FILE REFERENCE: 10793/44
;   CURRENT APPLICATION NUMBER: US/10/032,037B
;   CURRENT FILING DATE: 2001-12-31
;   PRIOR APPLICATION NUMBER: 60/258,948
;   PRIOR FILING DATE: 2000-12-29
;   NUMBER OF SEQ ID NOS: 204
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 87
;     LENGTH: 97
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-10-032-037B-87

Alignment Scores:
Pred. No.:                          0.00228        Length:           97
Score:                              98.20          Matches:          19
Percent Similarity:                 65.62%         Conservative:     2
Best Local Similarity:              59.38%         Mismatches:       3
Query Match:                        70.14%         Indels:           8
DB:                                 15             Gaps:             0

NOLAN463-1B.SEQ (1-81) x US-10-032-037B-87 (1-97)

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;   Sequence 87, Application US/10029988B
;   Publication No. US2004001833A1
;   GENERAL INFORMATION:
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;  APPLICANT: Bio-Technology General Corp.
;  TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
;  TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
;  FILE REFERENCE: 10793/46
;  CURRENT APPLICATION NUMBER: US/10/029,988B
;  CURRENT FILING DATE: 2001-12-31
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;  PRIOR FILING DATE: 2000-12-29
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;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-029-988B-87

Alignment Scores:
Pred. No.:                            Length:          97
Score:                  0.00228       Matches:         19
Percent Similarity:     98.20%        Conservative:    2
Best Local Similarity:  65.62%        Mismatches:      3
Query Match:            59.38%        Indels:          8
DB:                     70.14%        Gaps:            0
                        15

NOLAN463-1B.SEQ (1-81) x US-10-029-988B-87 (1-97)

Qy  2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT  61
           |||::: |||       |||||||||||||||||
Db 42  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  59

Qy 62  ACAACCCGTCCCTCAAGAGT  81
           ||||||||||||||||
Db 59  yrAsnProSerLeuLysSer  65
```

```
RESULT 9
US-10-032-423A-87
;  Sequence 87, Application US/10032423A
;  Publication No. US20040002450A1
;  GENERAL INFORMATION:
;  APPLICANT: Bio-Technology General Corp.
;  TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
;  TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
;  FILE REFERENCE: 10793/45
;  CURRENT APPLICATION NUMBER: US/10/032,423A
;  CURRENT FILING DATE: 2001-12-31
;  PRIOR APPLICATION NUMBER: 60/255,948
;  PRIOR FILING DATE: 12/29/2000
;  NUMBER OF SEQ ID NOS: 204
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 87
;  LENGTH: 97
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.:                            Length:          97
Score:                  0.00228       Matches:         19
Percent Similarity:     98.20%        Conservative:    2
Best Local Similarity:  65.62%        Mismatches:      3
Query Match:            59.38%        Indels:          8
DB:                     70.14%        Gaps:            0
                        15

NOLAN463-1B.SEQ (1-81) x US-10-032-423A-87 (1-97)

Qy  2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT  61
           |||::: |||       |||||||||||||||||
Db 42  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  59

Qy 62  ACAACCCGTCCCTCAAGAGT  81
           ||||||||||||||||
Db 59  yrAsnProSerLeuLysSer  65
```

```
RESULT 10
US-10-453-698-83
;  Sequence 83, Application US/10453698
;  Publication No. US20040038308A1
;  GENERAL INFORMATION:
;  APPLICANT: Rother, Russell
;  TITLE OF INVENTION: HYBRID ANTIBODIES
;  FILE REFERENCE: 82 CIP (1087-37 CIP)
;  CURRENT APPLICATION NUMBER: US/10/453,698
;  CURRENT FILING DATE: 2003-06-03
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 83
;  LENGTH: 97
;  TYPE: PRT
;  ORGANISM: human
US-10-453-698-83

Alignment Scores:
Pred. No.:                            Length:          97
Score:                  0.00228       Matches:         19
Percent Similarity:     98.20%        Conservative:    2
Best Local Similarity:  65.62%        Mismatches:      3
Query Match:            59.38%        Indels:          8
DB:                     70.14%        Gaps:            0
                        15

NOLAN463-1B.SEQ (1-81) x US-10-453-698-83 (1-97)

Qy  2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT  61
           |||::: |||       |||||||||||||||||
Db 42  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  59

Qy 62  ACAACCCGTCCCTCAAGAGT  81
           ||||||||||||||||
Db 59  yrAsnProSerLeuLysSer  65
```

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RESULT 11
US-10-029-926B-87
;  Sequence 87, Application US/10029926B
;  Publication No. US20040073011A1
;  GENERAL INFORMATION:
;  APPLICANT: HAGAY, et al.
;  TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
;  FILE REFERENCE: 10793/50
;  CURRENT APPLICATION NUMBER: US/10/029,926B
;  CURRENT FILING DATE: 2001-12-31
;  PRIOR APPLICATION NUMBER: 60/258,948
;  PRIOR FILING DATE: 12/29/2000
;  NUMBER OF SEQ ID NOS: 203
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 87
;  LENGTH: 97
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-029-926B-87

Alignment Scores:
Pred. No.:                            Length:          97
Score:                  0.00228       Matches:         19
Percent Similarity:     98.20%        Conservative:    2
Best Local Similarity:  65.62%        Mismatches:      3
Query Match:            59.38%        Indels:          8
DB:                     70.14%        Gaps:            0
                        15

NOLAN463-1B.SEQ (1-81) x US-10-029-926B-87 (1-97)

Qy  2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT  61
           |||::: |||       |||||||||||||||||
Db 42  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  59

Qy 62  ACAACCCGTCCCTCAAGAGT  81
           ||||||||||||||||
Db 59  yrAsnProSerLeuLysSer  65
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RESULT 12
US-10-379-392-47
; Sequence 47, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-47

Alignment Scores:
Pred. No.: 0.00228
Score: 98.20
Percent Similarity: 65.62%
Best Local Similarity: 59.38%
Query Match: 70.14%
DB: 16

NOLAN463-1B.SEQ (1-81) x US-10-379-392-47 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         ||| ||::: ||||||||||||||||||||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCCCTCAAGAGT 81
         ||||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 13
US-10-733-532-128
; Sequence 128, Application US/10733532
; Publication No. US20050026246A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2002B
; CURRENT APPLICATION NUMBER: US/10/733,532
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: PCT/GB02/02688
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 10/146,505
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-532-128

Alignment Scores:
Pred. No.: 0.00235
Score: 98.20
Percent Similarity: 65.62%
Best Local Similarity: 59.38%
Query Match: 70.14%
DB: 17

NOLAN463-1B.SEQ (1-81) x US-10-733-532-128 (1-114)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         ||| ||::: ||||||||||||||||||||||||||||||||||||
Db   36 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 53

Qy   62 ACAACCCGTCCCTCAAGAGT 81
         ||||||||||||||||||||
Db   53 yrAsnProSerLeuLysSer 59

RESULT 14
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US2005005642A1
; GENERAL INFORMATION:
; APPLICANT: GALIBERT, Laurent J.
; APPLICANT: YAN, Wei
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.: 0.00235
Score: 98.20
Percent Similarity: 65.62%
Best Local Similarity: 59.38%
Query Match: 70.14%
DB: 17

NOLAN463-1B.SEQ (1-81) x US-10-898-408-12 (1-115)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         ||| ||::: ||||||||||||||||||||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCCCTCAAGAGT 81
         ||||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 15
US-09-864-761-44315
; Sequence 44315, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366

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,   PRIOR FILING DATE: 2000-08-03
,   PRIOR APPLICATION NUMBER: GB 24263.6
,   PRIOR FILING DATE: 2000-10-04
,   PRIOR APPLICATION NUMBER: US 60/236,359
,   PRIOR FILING DATE: 2000-09-27
,   PRIOR APPLICATION NUMBER: PCT/US01/00666
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00667
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00664
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00669
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00665
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00668
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00663
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00662
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00661
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: PCT/US01/00670
,   PRIOR FILING DATE: 2001-01-30
,   PRIOR APPLICATION NUMBER: US 60/234,687
,   PRIOR FILING DATE: 2000-09-21
,   PRIOR APPLICATION NUMBER: US 09/608,408
,   PRIOR FILING DATE: 2000-06-30
,   PRIOR APPLICATION NUMBER: US 09/774,203
,   PRIOR FILING DATE: 2001-01-29
,   NUMBER OF SEQ ID NOS: 49117
,   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
,   SEQ ID NO 44315
,       LENGTH: 117
,       TYPE: PRT
,       ORGANISM: Homo sapiens
,       FEATURE:
,       OTHER INFORMATION: MAP TO AB019439.1
,       OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.54
,       OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.57
,       OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
,       OTHER INFORMATION: EST HUMAN HIT: BE672445.1, EVALUE 2.00e-57
,       OTHER INFORMATION: SWISSPROT HIT: P06331, EVALUE 1.00e-53
US-09-864-761-44315

Alignment Scores:
Pred. No.:                0.00236              Length:         117
Score:                    98.20                Matches:        19
Percent Similarity:       65.62%               Conservative:   2
Best Local Similarity:    59.38%               Mismatches:     3
Query Match:              70.14%               Indels:         8
DB:                       9                    Gaps:           0

NOLAN463-1B.SEQ (1-81) x US-09-864-761-44315 (1-117)

Qy     2  GGGCGAGTCAGGATATTAGCAGCTCGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT  61
          ||  ||::::  |||      || ||::   |||||||||||||||||||||||||||||||
Db    45  GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT   62

Qy    62  ACAACCCGTCCCTCAAGAGT  81
          ||||||||||||||||||||
Db    62  yrAsnProSerLeuLysSer  68

Search completed: August  4, 2005, 18:49:49
Job time : 81.25 secs
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:      August  4, 2005, 18:04:24 ; Search time 18.25 Seconds
                                      (without alignments)
                              854.089 Million cell updates/sec

Title:       NOLAN463-1B.SEQ
Perfect score: 140
Sequence:    1 CGGGCGAGTCAGGATATTAG........ACAACCCGTCCCTCAAGAGT 81

Scoring table: BLOSUM62
             Xgapop  10.0 , Xgapext   0.1
             Ygapop  10.0 , Ygapext   0.1
             Fgapop   6.0 , Fgapext   0.1
             Delop    6.0 , Delext    0.1

Searched:    283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
          1: pir1:*
          2: pir2:*
          3: pir3:*
          4: pir4:*

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-1/runat_04082005_125806_24544/app_query.fasta_1.5
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN 1 1 77 @runat_04082005_125806_24544 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	101.6	72.6	143	2	B49028	Ig heavy chain V-I
2	100.4	71.7	97	2	S26805	Ig heavy chain V r
3	98.2	70.1	97	2	S26898	Ig heavy chain V r
4	98.2	70.1	97	2	S26806	Ig heavy chain V r
5	98.2	70.1	106	2	S37454	Ig mu chain - huma
6	98.2	70.1	122	2	JL0047	Ig heavy chain V r
7	98.2	70.1	126	2	S47010	Ig heavy chain V4.
8	98.2	70.1	140	2	S78052	Ig heavy chain pre
9	98.2	70.1	140	2	A49045	Ig heavy chain V r
10	98.2	70.1	231	2	B23746	Ig Fab region IV-J
11	98	70.0	133	2	PS0341	Ig heavy chain V-D
12	94.2	67.3	97	2	G34964	Ig heavy chain V-I
13	92	65.7	98	2	S26905	Ig heavy chain V r
14	92	65.7	145	2	S78055	Ig heavy chain pre

15	89.2	63.7	97	2	S14474	Ig heavy chain V r
16	88	62.9	129	2	S44114	Ig heavy chain V r
17	87.2	62.3	146	1	G1HUH2	Ig heavy chain pre
18	86.2	61.6	134	2	S54906	Ig heavy chain V r
19	86	61.4	98	2	S26904	Ig heavy chain V r
20	83.7	59.8	134	2	B24672	Ig heavy chain pre
21	83.2	59.4	114	2	I72667	cold agglutinin FS
22	83	59.3	123	2	S30529	Ig heavy chain V r
23	81.2	58.0	97	2	JH0428	Ig gamma chain V r
24	80.3	57.4	116	2	S38718	Ig heavy chain V r
25	80.1	57.2	98	2	S26902	Ig heavy chain V r
26	80.1	57.2	98	2	S12221	Ig heavy chain V r
27	80.1	57.2	130	2	S31673	Ig heavy chain V r
28	80.1	57.2	140	2	A24770	hypothetical hybri
29	79.9	57.1	127	2	S19668	Ig heavy chain V r
30	79.1	56.5	97	2	S26906	Ig heavy chain V r
31	79.1	56.5	97	2	S12416	Ig heavy chain V r
32	79.1	56.5	105	2	S44125	Ig lambda chain V
33	79.1	56.5	130	2	S31690	Ig heavy chain V r
34	79.1	56.5	140	2	I37782	Ig variable region
35	78.9	56.4	99	2	S12412	Ig heavy chain V r
36	78.3	55.9	106	2	S26464	Ig heavy chain V r
37	78.1	55.8	116	2	B26340	Ig heavy chain pre
38	77.9	55.6	118	2	A26340	Ig heavy chain pre
39	77.6	55.4	109	2	PH1673	Ig heavy chain V r
40	77.2	55.1	97	2	PL0118	Ig heavy chain V-I
41	77.2	55.1	99	2	S26899	Ig heavy chain V r
42	77.2	55.1	130	2	S30534	Ig heavy chain V r
43	77.1	55.1	97	2	S26804	Ig heavy chain V r
44	77.1	55.1	97	2	S26808	Ig heavy chain V r
45	77.1	55.1	116	2	S18557	Ig heavy chain V r

ALIGNMENTS

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RESULT 1
B49028
Ig heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur.
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: B49028
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-143 <TIM>
A;Cross-references: GB:S64473; NID:g236906; PIDN:AAB20012.1; PID:g236907
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:             0.000109        Length:           143
Score:                 101.60          Matches:          19
Percent Similarity:    55.56%          Conservative:     1
Best Local Similarity: 52.78%          Mismatches:       2
Query Match:           72.57%          Indels:           14
DB:                    2               Gaps:             0

NOLAN463-1B.SEQ (1-81) x B49028 (1-143)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCAATCAGTGGAAGCACCAACT  61
             |||||          |||:::       ||||||||||||||||||
Db   44 GlyArg--------------GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  59

Qy   62 ACAACCCGTCCCTCAAGAGT  81
             ||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer  65
```

RESULT 2
S26805
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000153   Length: 97
Score: 100.40   Matches: 20
Percent Similarity: 43.40%   Conservative: 4
Best Local Similarity: 37.74%   Mismatches: 26
Query Match: 71.71%   Indels: 1
DB: 2   Gaps: 2

NOLAN463-1B.SEQ (1-81) x S26805 (1-97)

Qy   1 CGGGCGAGTCAGGATATTAGC-------------------------   21
          ::: ||||| :::|||
Db 13 LysProSerGlnThrLeuThrCysAlaAlaValTyrGlyGlySerPheSerGlyTyr   32

Qy 22 -------------------------------AGCTGGTTAGCCGAAATCAAT   42
                                        |||||: |||||||||
Db 33 TyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGluAsn   52

Qy 43 CATAGTGGAAGCACCAACTACAACCCGTCCTCAAGAGT   81
        |||||||||||||||||||||||||||||||||
Db 53 HisSerGlySerThrAsnTyrAsnProSerLeuLysSer   65

RESULT 3
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898; S12420
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V(H)
J. Mol. Biol. 227, 776-798, 1992
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26898
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
A;Experimental source: clone DP-63
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12420
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <SAN>
A;Cross-references: EMBL:X56364
A;Experimental source: V(H)4.2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000295   Length: 97

Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 2   Gaps: 0

NOLAN463-1B.SEQ (1-81) x S26898 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||:::| ||| |||||: ||||||||||||
Db 42 GlyLys---GlyLeu---GluTrpIleGlyIleGluAsnHisSerGlySerThrAsnT   59

Qy 62 ACAACCCGTCCTCAAGAGT   81
        |||||||||||||||||
Db 59 yrAsnProSerLeuLysSer   65

RESULT 4
S26806
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26806
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000295   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 2   Gaps: 0

NOLAN463-1B.SEQ (1-81) x S26806 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||:::| ||| |||||: ||||||||||||
Db 42 GlyLys---GlyLeu---GluTrpIleGlyIleGluAsnHisSerGlySerThrAsnT   59

Qy 62 ACAACCCGTCCTCAAGAGT   81
        |||||||||||||||||
Db 59 yrAsnProSerLeuLysSer   65

RESULT 5
S37454
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from ...
submitted to the EMBL Data Library, September 1993
A;Reference number: S37453
A;Accession: S37454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>
A;Cross-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Alignment Scores:
Pred. No.:   0.000297   Length: 106

```
Score:                  98.20           Matches:        19
Percent Similarity:     65.62%          Conservative:   2
Best Local Similarity:  59.38%          Mismatches:     3
Query Match:            70.14%          Indels:         8
DB:                                     Gaps:           0

NOLAN463-1B.SEQ (1-81) x S37454 (1-106)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
          ||:::    ||       ||||||||||||||||||||||||||
Db   20 GlyLys---GluLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 37

Qy   62 ACAACCGTCCCTCAAGAGT 81
          |||||||||||||||||
Db   37 yrAsnProSerLeuLysSer 43

RESULT 6
JL0047
Ig heavy chain V region precursor (clone cR18) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: JL0047
R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new S
A;Reference number: JL0047; MUID:88258392; PMID:3133445
A;Accession: JL0047
A;Molecule type: mRNA
A;Residues: 1-122 <BAE>
A;Experimental source: T-cell line RPMI 8402
A;Note: the authors translated the reading frame which extends to the stop codon; the se
A;Note: this sequence belongs to the VH II subgroup
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.000299        Length:         122
Score:                  98.20           Matches:        19
Percent Similarity:     65.62%          Conservative:   2
Best Local Similarity:  59.38%          Mismatches:     3
Query Match:            70.14%          Indels:         8
DB:                                     Gaps:           0

NOLAN463-1B.SEQ (1-81) x JL0047 (1-122)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
          ||:::    |||      ||||||||||||||||||||||||||
Db   50 GlyLys---GluLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 67

Qy   62 ACAACCGTCCCTCAAGAGT 81
          |||||||||||||||||
Db   67 yrAsnProSerLeuLysSer 73

RESULT 7
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S47010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A;Reference number: S47009
A;Accession: S47010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
```

```
Alignment Scores:
Pred. No.:              0.0003          Length:         126
Score:                  98.20           Matches:        19
Percent Similarity:     65.62%          Conservative:   2
Best Local Similarity:  59.38%          Mismatches:     3
Query Match:            70.14%          Indels:         8
DB:                                     Gaps:           0

NOLAN463-1B.SEQ (1-81) x S47010 (1-126)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGAAGCACCACT 61
          ||||:    |||      ||||||||||||||||||||||||||
Db   42 GlyLys---GluLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCGTCCCTCAAGAGT 81
          |||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 8
S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052, S23717
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:              0.000301        Length:         140
Score:                  98.20           Matches:        19
Percent Similarity:     65.62%          Conservative:   2
Best Local Similarity:  59.38%          Mismatches:     3
Query Match:            70.14%          Indels:         8
DB:                                     Gaps:           0

NOLAN463-1B.SEQ (1-81) x S78052 (1-140)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGAAGCACCACT 61
          ||:::    |||      ||||||||||||||||||||||||||
Db   56 GlyLys---GluLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 73

Qy   62 ACAACCGTCCCTCAAGAGT 81
          |||||||||||||||||
Db   73 yrAsnProSerLeuLysSer 79

RESULT 9
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
```

A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <GRI>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:                0.000301      Length:        140
Score:                    98.20         Matches:        19
Percent Similarity:       65.62%        Conservative:    3
Best Local Similarity:    59.38%        Mismatches:      8
Query Match:              70.14%        Indels:          0
                                        Gaps:            0
```

NOLAN463-1B.SEQ (1-81) x A49045 (1-140)

```
Qy   2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
           |||.:::  ||  ||||||||||||||||||||
Db  61  GlyLeu---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78

Qy  62  ACAACCGTCCCTCAAGAGT 81
        |||||||||||||||||
Db  78  yrAsnProSerLeuLysSer 84
```

RESULT 10
B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: B23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:                0.00031       Length:        231
Score:                    98.20         Matches:        19
Percent Similarity:       65.62%        Conservative:    2
Best Local Similarity:    59.38%        Mismatches:      3
Query Match:              70.14%        Indels:          8
                                        Gaps:            0
```

NOLAN463-1B.SEQ (1-81) x B23746 (1-231)

```
Qy   2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
           |||.:::  ||  ||||||||||||||||||||
Db  41  GlyLeu---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 58

Qy  62  ACAACCGTCCCTCAAGAGT 81
        |||||||||||||||||
Db  58  yrAsnProSerLeuLysSer 64
```

RESULT 11
PS0341
Ig heavy chain V-D-J region (RAMOS) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C;Accession: PS0341
R;Ratech, H.
Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell

A;Reference number: PS0341; MUID:92171937; PMID:1540170
A;Accession: PS0341
A;Molecule type: mRNA
A;Residues: 1-113 <RAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-38/Region: framework 1
F;39-43/Region: complementarity-determining 1
F;44-57/Region: framework 2
F;58-74/Region: complementarity-determining 2
F;75-106/Region: framework 3

```
Alignment Scores:
Pred. No.:                0.000319      Length:        133
Score:                    98.00         Matches:        17
Percent Similarity:       94.74%        Conservative:    1
Best Local Similarity:    89.47%        Mismatches:      1
Query Match:              70.00%        Indels:          0
                                        Gaps:            0
```

NOLAN463-1B.SEQ (1-81) x PS0341 (1-133)

```
Qy  25  TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAAGAGT 81
        |||.:::   |||||||||||||||||||||||||||||||||
Db  55  TrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer 73
```

RESULT 12
G34964
Ig heavy chain V-IV region (AB44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
A;Molecule type: mRNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:                0.000978      Length:         97
Score:                    94.20         Matches:        18
Percent Similarity:       62.50%        Conservative:    2
Best Local Similarity:    56.25%        Mismatches:      4
Query Match:              67.29%        Indels:          8
                                        Gaps:            0
```

NOLAN463-1B.SEQ (1-81) x G34964 (1-97)

```
Qy   2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
           |||.:::   |||||||||||||||||||
Db  42  GlyLeu---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlyGlyThrAsnT 59

Qy  62  ACAACCGTCCCTCAAGAGT 81
        ||||||||||||
Db  59  yrAsnProSerLeuLysSer 65
```

RESULT 13
S26905
Ig heavy chain V region (DP-70 / 4.19) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12419
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <SAN>
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00189   Length: 98
Score: 92.00   Matches: 21
Percent Similarity: 48.89%   Conservative: 1
Best Local Similarity: 46.67%   Mismatches: 3
Query Match: 65.71%   Indels: 20
DB: Gaps: 1

NOLAN463-1B.SEQ (1-81) x S26905 (1-98)

Qy   3 GGCGGAGTCAGGATATTAGCAGC------------------------------- 24
          ||| ||| |||||||||
Db   26 GlyGlySer---IleSerSerSerAsnTrpSerTrpSerValArgGlnProGlyLy 44

Qy   25 --------TGGTTAGCCGAAATCAATCATCATGTGGAAGGACCACCAACTACAACCCGTCCCT 74
                  ||::: |||||||||||||||||||||||||||||
Db   44 sGlyLeuGluTrpIleGlyLeuIleTyrHisSerGlySerThrAsnTyrAsnProSerLe 64

Qy   75 CAAGAGT 81
          |||||||
Db   64 uLysSer 66

RESULT 14
S78055
Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78055; S23720
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78055
A;Molecule type: mRNA
A;Residues: 1-145 <HAR>
A;Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23720
A;Molecule type: mRNA
A;Residues: 18-115 <HAW>
A;Cross-references: EMBL:X54445
A;Note: the authors translated the codon GCA for residue 67 as Arg
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F;18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00193   Length: 145
Score: 92.00   Matches: 21

Percent Similarity: 48.89%   Conservative: 1
Best Local Similarity: 46.67%   Mismatches: 3
Query Match: 65.71%   Indels: 20
DB: Gaps: 1

NOLAN463-1B.SEQ (1-145) x S78055 (1-145)

Qy   3 GGCGGAGTCAGGATATTAGCAGC------- 24
          ||| |||||||||
Db   43 GlyGlySer----IleSerSerSerAsnTrpTrpSerTrpValArgGlnProGlyLy 61

Qy   25 --------TGGTTAGCCGAAATCAATCATCATGTGGAAGGACCACCAACTACAACCCGTCCT 74
                  ||::: ||||||||||||||||||||||||||
Db   61 sGlyLeuGluTrpIleGlyLeuIleTyrHisSerGlySerThrAsnTyrAsnProSerIle 81

Qy   75 CAAGAGT 81
          |||||||
Db   81 uLysSer 83

RESULT 15
S14474
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S14474
R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H
submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Accession: S14474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <ESJ>
A;Cross-references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:g1335354
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00437   Length: 97
Score: 89.20   Matches: 18
Percent Similarity: 62.50%   Conservative: 2
Best Local Similarity: 56.25%   Mismatches: 4
Query Match: 63.71%   Indels: 8
DB: Gaps: 0

NOLAN463-1B.SEQ (1-81) x S14474 (1-97)

Qy   2 GGGCGGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATGGAAGGACCAACT 61
          ||::: ||||| |||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyIleIleHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCCCTCAAGAGT 81
          ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

Search completed: August 4, 2005, 18:21:23
Job time : 18.25 secs

```
                GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August 4, 2005, 17:55:57 ; Search time 83.75 Seconds
                                       (without alignments)
                                       990.529 Million cell updates/sec

Title:        NOLAN463-1B.SEQ
Perfect score: 140
Sequence:     1 CGGGCGAGTCAGGATATTAG........ACAACCCGTCCCTCAAGAGT 81

Scoring table: BLOSUM62
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           Ygapop 10.0 , Ygapext  0.1
           Fgapop  6.0 , Fgapext  0.1
           Delop   6.0 , Delext   0.1

Searched:     1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:          3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-1/runat_04082005_125806_24533/app_query.fasta_1.5
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN_1_1_305 @runat_04082005_125806_24533 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :   UniProt_03:*
           1: uniprot_sprot:*
           2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	98.2	70.1	116	2	Q7Z3Y6	Q7Z3Y6 homo sapien
2	98.2	70.1	595	2	Q8WUX4	Q8WUX4 homo sapien
3	98.2	70.1	597	2	Q6GMX5	Q6GMX5 homo sapien
4	98.2	70.1	597	2	Q9BU10	Q9BU10 homo sapien
5	98.2	70.1	625	2	Q96AA6	Q96AA6 homo sapien
6	92	65.9	597	2	Q9BQB8	Q9BQB8 homo sapien
7	92	65.7	576	2	Q6P4I8	Q6P4I8 homo sapien
8	87.2	62.3	146	1	HV2I_HUMAN	HV2I_HUMAN homo sapien
9	82.1	58.6	477	2	Q6GMX7	Q6GMX7 homo sapien
10	79.1	56.5	139	2	Q86SX2	Q86SX2 homo sapien
11	77.1	55.1	620	2	Q96EY0	Q96EY0 homo sapien
12	76.3	54.5	479	2	Q99M22	Q99M22 mus musculu
13	75.7	54.1	116	1	HV61_MOUSE	HV61_MOUSE mus musculu
14	75.2	53.7	465	2	Q6GMX6	Q6GMX6 homo sapien
15	72.8	52.0	262	2	Q65ZI1	Q65ZI1 mus musculu
16	71.3	50.9	116	1	HV60_MOUSE	HV60_MOUSE mus musculu
17	71.2	50.9	119	2	Q9UL73	Q9UL73 homo sapien
18	71.2	50.9	476	2	Q6GMX1	Q6GMX1 homo sapien
19	69.1	49.4	478	2	Q6NYH3	Q6NYH3 homo sapien
20	68.6	49.0	150	2	O95973	O95973 homo sapien
21	68.2	48.7	478	2	Q72379	Q72379 homo sapien
22	67.4	48.1	113	1	HV47_MOUSE	HV47_MOUSE mus musculu
23	66.4	47.4	104	2	Q99CA9	Q99CA9 human immun
24	66.4	47.4	106	2	Q6TIQ4	Q6TIQ4 human immun
25	66.4	47.4	133	2	Q90QV6	Q90QV6 human immun
26	65.9	47.1	496	2	Q96KX8	Q96KX8 homo sapien
27	65.5	46.8	523	2	Q6QJ60	Q6QJ60 paraphlegop
28	65.5	46.8	523	2	Q6QJ62	Q6QJ62 paraphlegop
29	65.4	46.7	104	2	Q99CH3	Q99CH3 human immun
30	65.4	46.7	130	2	Q9QL43	Q9QL43 human immun
31	65.4	46.7	202	2	Q9IUP1	Q9IUP1 human immun
32	65.4	46.7	202	2	Q9IUR6	Q9IUR6 human immun
33	65.4	46.7	206	2	Q7ZN97	Q7ZN97 human immun
34	65.4	46.7	207	2	Q9IUQ5	Q9IUQ5 human immun
35	65.4	46.7	212	2	Q9J783	Q9J783 human immun
36	65.4	46.7	220	2	Q9IUT6	Q9IUT6 human immun
37	65.4	46.7	231	2	Q9IQS9	Q9IQS9 human immun
38	65.4	46.7	489	2	Q80632	Q80632 human immun
39	65.3	46.6	136	2	Q6LBQ5	Q6LBQ5 mus musculu
40	65.3	46.6	137	1	HV46_MOUSE	HV46_MOUSE mus musculu
41	64.4	46.0	130	2	Q7ZB82	Q7ZB82 human immun
42	64.4	46.0	131	2	Q90QT5	Q90QT5 human immun
43	64.4	46.0	131	2	Q90KY2	Q90KY2 human immun
44	64.4	46.0	131	2	Q90KY3	Q90KY3 human immun
45	64.4	46.0	140	2	Q69BZ8	Q69BZ8 human immun

ALIGNMENTS

```
RESULT 1
Q7Z3Y6
ID   Q7Z3Y6        PRELIMINARY;      PRT;   116 AA.
AC   Q7Z3Y6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rearranged VH4-34 V gene segment (Fragment).
GN   Name=VH4-34;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564425; CAD92032.1; -.
DR   HSSP; P18532; 1KCV.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1          1
FT   NON_TER       116        116
SQ   SEQUENCE   116 AA;  12902 MW;  CE3D8A846616C908 CRC64;

Alignment Scores:
Pred. No.:              0.000788
Score:                  98.20
Percent Similarity:     65.62%        Length:         116
Best Local Similarity:  59.38%        Matches:        19
Query Match:            70.14%        Conservative:   2
DB:                     2             Mismatches:     3
                                      Indels:         8
                                      Gaps:           0

NOLAN463-1B.SEQ (1-81) x Q7Z3Y6 (1-116)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAAGCACCAACT 61
```

```
Db          42 GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
               |||::: |||        |||||||||||||||||||||||||||||
Qy          62 ACAACCGTCCCTCAAGAGT 81
               ||||||||||||||||||
Db          59 yrAsnProSerLeuLysSer 65
```

```
Qy          62 ACAACCGTCCCTCAAGAGT 81
               ||||||||||||||||||
Db          85 yrAsnProSerLeuLysSer 91
```

RESULT 3
Q6GMX5
ID   Q6GMX5   PRELIMINARY;   PRT;   597 AA.
AC   Q6GMX5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073767; AAH73767.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003396; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Alignment Scores:
Pred. No.:   0.000979   Length: 597
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
                                                    Gaps: 0

NOLAN463-1B.SEQ (1-81) x Q6GMX5 (1-597)

Qy   2 GGGGGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
```

RESULT 2
Q8WUX4
ID   Q8WUX4   PRELIMINARY;   PRT;   595 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019235; AAH19235.2; -.
PIR; G34964; G34964.
HSSP; P01861; 1ADQ.
Pfam; PF07654; C1-set; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE 595 AA; 65290 MW; 0D4B5077654571AE CRC64;

Alignment Scores:
Pred. No.:   0.000979   Length: 595
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
                                                    Gaps: 0

NOLAN463-1B.SEQ (1-81) x Q8WUX4 (1-595)

```
Qy           2 GGGGGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
               |||::: |||        |||||||||||||||||||||||||||||
Db          68 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 85
```

```
Db           |||:::  |||     |||:::   |||||||||||||||
          61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78

Qy        62 ACAACCGTCCTCAAGAGT 81
             |||||||||||||||||
Db        78 yrAsnProSerLeuLysSer 84

RESULT 4
Q9BU10
ID   Q9BU10;           PRELIMINARY;     PRT;    597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE  597 AA;  65274 MW;  2DAFA8FB7B055851 CRC64;

Alignment Scores:
Pred. No.:              0.000979      Length:            597
Score:                 98.20         Matches:           19
Percent Similarity:    65.62%        Conservative:      2
Best Local Similarity: 59.38%        Mismatches:        3
Query Match:           70.14%        Indels:            8
DB:                    2             Gaps:              0

NOLAN463-1B.SEQ (1-81) x Q9BU10 (1-597)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         |||:::  |||     |||:::   |||||||||||||||
Db   61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
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```
Qy        62 ACAACCGTCCTCAAGAGT 81
             |||||||||||||||||
Db        78 yrAsnProSerLeuLysSer 84

RESULT 5
Q96AA6
ID   Q96AA6;           PRELIMINARY;     PRT;    625 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.2; -.
DR   PIR; S15590; S15590.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE  625 AA;  68610 MW;  F62FAB3ADE7ECBFE CRC64;

Alignment Scores:
Pred. No.:              0.000985      Length:            625
Score:                 98.20         Matches:           19
Percent Similarity:    65.62%        Conservative:      2
Best Local Similarity: 59.38%        Mismatches:        3
Query Match:           70.14%        Indels:            8
DB:                    2             Gaps:              0

NOLAN463-1B.SEQ (1-81) x Q96AA6 (1-625)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
```

```
Db        68  GlyLys---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT   85
              |||::  :       |||         |||||||||||||||||||||||
Qy        62  ACAACCGTCCCTCAAGAGT                                  81
              ||||||||||||||||||
Db        85  yrAsnProSerLeuLysSer   91
```

```
RESULT 6
Q9BQB8
ID   Q9BQB8        PRELIMINARY;      PRT;    597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE  597 AA;  65300 MW;  2DAFAD50A6375851 CRC64;

Alignment Scores:
Pred. No.:                 0.00622         Length:            597
Score:                     92.20           Matches:           18
Percent Similarity:        62.50%          Conservative:      2
Best Local Similarity:     56.25%          Mismatches:        4
Query Match:               85.86%          Indels:            8
DB:                        2               Gaps:              0

NOLAN463-1B.SEQ (1-81) x Q9BQB8 (1-597)

Qy         2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT   61
              ||::     |||         |||:::    |||||||||||||||||||||||||||||
Db        61  GlyLys---GluTrpIleGlyGluIleAsnHisSerGlyIleThrAsnT   78
```

```
Db        62  ACAACCGTCCCTCAAGAGT   81
              |||||||||||||||||||
Qy        85  yrAsnProSerLeuLysSer   91
```

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RESULT 7
Q6P4I8
ID   Q6P4I8        PRELIMINARY;      PRT;    576 AA.
AC   Q6P4I8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHD protein.
GN   Name=IGHD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063384; AAH63384.1; -.
HSSP; P01820; 1A7N.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ   SEQUENCE  576 AA;  63363 MW;  FBB97C949D720F1E CRC64;

Alignment Scores:
Pred. No.:                 0.00658         Length:            576
Score:                     92.00           Matches:           21
Percent Similarity:        48.89%          Conservative:      1
Best Local Similarity:     46.67%          Mismatches:        3
Query Match:               65.71%          Indels:            20
DB:                        1               Gaps:              1

NOLAN463-1B.SEQ (1-81) x Q6P4I8 (1-576)
```

Qy   3 GGCCGAGTCAGGATATTAGCAGC------------------------ 24
           ||||||| |||
Db   52 GlyGlySer---IleSerSerSerAsnTrpTrpSerValArgGlnProProGlyLy 70

Qy   25 ------TGGTTAGCCGAAATCAATCAATCATAGTGGAAGCACCAACCGTCCCT 74
           |||::: ||||||||||||||||||||||||||||||||||||||||||||
Db   70 sGlyLeuTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLe 90

Qy   75 CAAGAGT 81
           |||||||
Db   90 uLysSer 92

RESULT 8
HV2I_HUMAN
ID   HV2I_HUMAN   STANDARD;   PRT;   146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; G1HUH2.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   146   Ig heavy chain V-II region ARH-77.
FT   DOMAIN   20   117   V segment.
FT   DOMAIN   118   127   D segment.
FT   DOMAIN   128   146   J segment.
FT   DISULFID   42   115   By similarity.
FT   NON_TER   146   146
SQ   SEQUENCE   146 AA;   16228 MW; 8D7FD52BB218171F CRC64;

Alignment Scores:
Pred. No.:   0.024   Length: 146
Score: 87.20   Matches: 18
Percent Similarity: 59.38%   Conservative: 1
Best Local Similarity: 56.25%   Mismatches: 5
Query Match: 62.29%   Indels: 8
DB: 1   Gaps: 0

NOLAN463-1B.SEQ (1-81) x HV2I_HUMAN (1-146)

Qy   2 GGCCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCAATCATAGTGGAAGCACCAACT 61
           ||||||| ||| |||| |||||||||||||||||||||||||||
Db   62 GlyArg----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 79

Qy   62 ACAACCGTCCCTCAAGAGT 81
           || |||||||||||
Db   79 yrLysThrSerLeuLysSer 85

RESULT 9
Q6GMX7
ID   Q6GMX7   PRELIMINARY;   PRT;   477 AA.
AC   Q6GMX7;

DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073765; AAH73765.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   477 AA;   51631 MW; 9FE59C09C50CFF85 CRC64;

Alignment Scores:
Pred. No.:   0.135   Length: 477
Score: 82.10   Matches: 19
Percent Similarity: 47.73%   Conservative: 2
Best Local Similarity: 43.18%   Mismatches: 4
Query Match: 58.64%   Indels: 19
DB: 2   Gaps: 1

NOLAN463-1B.SEQ (1-81) x Q6GMX7 (1-477)

Qy   3 GGCCGAGTCAGGATATTAGCAGC------------------------ 24
           ||||||| |||
Db   3 GlyGlySer----IleSerSerTyrTyrTrpSerTrpIleArgGlnThrAlaGlyLysG1 45

Qy   25 ------TGGTTAGCCGAAATCAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAA 77
           |||::: ||||||||||||||||||||||||||||||||||||||||||||
Db   45 yLeuGluTrpIleGlyTyrIleSerHisSerGlySerThrThrTyrAsnProSerLeuLysY 83

Qy   78 GAGT 81
           ||||
Db   78

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Db        83 sSer 84

RESULT 10
Q86SX2
ID   Q86SX2        PRELIMINARY;      PRT;   139 AA.
AC   Q86SX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE   Homo sapiens (human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248300; CAD62627.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1
SQ   SEQUENCE   139 AA;  15573 MW;  7D1E2302410E4F8C CRC64;

Alignment Scores:
Pred. No.:                 0.289      Length:        139
Score:                    79.10      Matches:        19
Percent Similarity:       47.73%     Conservative:    2
Best Local Similarity:    43.18%     Mismatches:      4
Query Match:              56.50%     Indels:         19
DB:                       2          Gaps:            1

NOLAN463-1B.SEQ (1-81) x Q86SX2 (1-139)

Qy    3 GGCGAGTCAGGATATTAGCAGC----------------------------- 24
        |||.||||||||||||||||||
Db   58 GlyGlySer-----IleSerSerTyrTyrTrpSerTyrIleArgGlnProProGlyLysGl 76

Qy   25 ------TGGTTAGCCGAAATCAATCATGATGGAAGCACCAACTACACCCGTCCCTCAA 77
        |||.::|  ||||||||||||||||||||||||||||||||||||
Db   76 yLeuGluTrpIleGlyArgIleTyrTyrSerGlySerThrAsnTyrAsnProSerLeuLy 96

Qy   78 GAGT 81
        ||||
Db   96 sSer 97

RESULT 11
Q96EY0
ID   Q96EY0        PRELIMINARY;      PRT;   620 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.2; -.
DR   PIR; S15590; S15590.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3
SQ   SEQUENCE   620 AA;  68125 MW;  990A1A4A6E8FF27B CRC64;

Alignment Scores:
Pred. No.:                 0.654      Length:        620
Score:                    77.10      Matches:        19
Percent Similarity:       45.45%     Conservative:    1
Best Local Similarity:    43.18%     Mismatches:      5
Query Match:              55.07%     Indels:         19
DB:                       2          Gaps:            1

NOLAN463-1B.SEQ (1-81) x Q96EY0 (1-620)

Qy    3 GGCGAGTCAGGATATTAGCAGC----------------------------- 24
        |||.||| |||||||||||||
Db   52 GlyGlySer-----IleSerSerTyrTyrTrpSerTyrIleArgGlnProAlaGlyLysGl 70

Qy   25 ------TGGTTAGCCGAAATCAATCATGATGGAAGCACCAACTACACCCGTCCCTCAA 77
        |||      ||||||||||||||||||||||||||||||||||||
Db   70 yLeuGluTrpIleGlyArgIleTyrTyrSerGlySerThrAsnTyrAsnProSerLeuUy 90

Qy   78 GAGT 81
        ||||
Db   90 sSer 91

RESULT 12
Q99M22
ID   Q99M22        PRELIMINARY;      PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE 479 AA; 51992 MW; 768E39A13918892 CRC64;

Alignment Scores:
Pred. No.:   0.808
Score: 76.30
Percent Similarity: 37.04%
Best Local Similarity: 27.78%
Query Match: 54.50%
DB: 2

Length: 479
Matches: 15
Conservative: 5
Mismatches: 7
Indels: 27
Gaps: 1

NOLAN463-1B.SEQ (1-81) x Q99M22 (1-479)

Qy   1 CGGCGAGTCAGGATATTAGC----------------------------------- 21
         ::: ||||||| ::|||
Db   31 LysProSerGlnSerLeuSerLeuThrCysSerValThrGlyTyrSerIleThrSerGly 50

Qy   22 --AGCTGGTTAGCCGAAATC 39
                                                   ||:::
Db   51 TyrTyrTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 70

Qy   40 AATCATAGTGGAAGCACCAACTACAACCCGTCCTCAAGAGT 81
          |||::: |||||| ||||||||||||||||||||||||:::
Db   71 AsnTyrAspGlySerAsnAsnTyrAsnProSerLeuLysAsn 84

RESULT 13
HV61_MOUSE
ID   HV61_MOUSE   STANDARD;   PRT;   116 AA.
AC   P18532;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region 1B43 precursor.

OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during the
RT   primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
DR   PIR; JT0508; HVMS1B.
DR   PDB; 1KCS; X-ray; H=19-116.
DR   PDB; 1KCV; X-ray; H=19-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin V region; Signal.
FT   SIGNAL   1   18
FT   CHAIN   19   116   Ig heavy chain V region 1B43
FT   DOMAIN   19   48   Framework-1.
FT   DOMAIN   49   53   Complementarity-determining-1.
FT   DOMAIN   54   67   Framework-2.
FT   DOMAIN   68   84   Complementarity-determining-2.
FT   DOMAIN   85   116   Framework-3.
FT   DISULFID   40   114   By similarity.
FT   STRAND   21   25
FT   STRAND   29   30
FT   TURN   32   33
FT   STRAND   36   43
FT   TURN   47   49
FT   STRAND   52   58
FT   TURN   60   61
FT   STRAND   64   71
FT   TURN   72   73
FT   STRAND   76   78
FT   TURN   80   85
FT   STRAND   86   91
FT   TURN   92   95
FT   STRAND   96   101
FT   HELIX   106   108
FT   STRAND   110   116
FT   NON_TER   116   116
SQ   SEQUENCE   116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Alignment Scores:
Pred. No.:   0.805
Score: 75.70
Percent Similarity: 56.76%
Best Local Similarity: 43.24%
Query Match: 54.07%
DB: 1

NOLAN463-1B.SEQ (1-81) x HV61_MOUSE (1-116)

Length: 116
Matches: 16
Conservative: 5
Mismatches: 3
Indels: 13
Gaps: 1

Qy   9 TCAGGATATTAGC-------------------------------AGCTGGTTAGC 32
         ||||||||| ||| ||:::
Db   49 SerGlyTyr-SerTrpHisTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGl 68

Qy   33 CGAAATCAATCATCATAGTGGAAGCACCAACTACAACCCGTCCTCAAGAGT 81
         |||:::||||:::||||||||:::||||||||::||||||||||||||||||
Db   68 yTyrIleHisTyrSerGlyAsnThrSerTyrAsnProSerLeuLysSer 84

RESULT 14
Q6GMX6
ID   Q6GMX6   PRELIMINARY;   PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

```
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;
```

Alignment Scores:
```
Pred. No.:                   1.13
Score:                      75.20
Percent Similarity:         56.25%
Best Local Similarity:      50.00%
Query Match:                53.71%
DB:                         2
```

```
Length:          465
Matches:          16
Conservative:      2
Mismatches:        6
Indels:            8
Gaps:              0
```

NOLAN463-1B.SEQ (1-81) x Q6GMX6 (1-465)

```
Qy     2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGGAAGCACCAACT 61
           |||::::  |||      |||::::  |||:    ||||||||||||||||||||||
Db    61 GlyLys----GlyLeu---GluTrpIleGlyArgIleTyrThrSerGlySerThrAsnT 78

Qy    62 ACAACCCGTCCCTCAAGAGT 81
          ||||||||||||||||||||
Db    78 yrAsnProSerLeuLysSer 84
```

```
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Anti-HIV-1 reverse transcriptase single-chain variable.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hybridoma;
RX   MEDLINE=96211469; PubMed=8648670;
RA   Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
RT   "Targeting human immunodeficiency virus type 1 reverse transcriptase
RT   by intracellular expression of single-chain variable fragments to
RT   inhibit early stages of the viral life cycle.";
RL   J. Virol. 70:3392-3400(1996).
DR   EMBL; U48716; AAB64342.1; -.
DR   GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   RNA-directed DNA polymerase.
SQ   SEQUENCE   262 AA;  27842 MW;  7DF20138E53865E4 CRC64;
```

Alignment Scores:
```
Pred. No.:                   2.19
Score:                      72.80
Percent Similarity:         55.56%
Best Local Similarity:      44.44%
Query Match:                52.00%
DB:                         2
```

```
Length:          262
Matches:          16
Conservative:      4
Mismatches:        4
Indels:           12
Gaps:              1
```

NOLAN463-1B.SEQ (1-81) x Q65ZI1 (1-262)

```
Qy     9 TCAGGATATTAGCAGCTCGTTAGCCGAA----------------------------- 36
           |||||||||    ::||||:     :::|||
Db   178 SerGlyTyr-TrpAsnTrpIleArgLysPheProGlyAsnLysLysAspTyrMetGlyTy 197

Qy    37 -ATCAATCATAGTCGGAAGCACCACAACTACAACCCGTCCCTCAAGAGT 81
          |||||:::||||||      |||   |||||||||||||||||||||
Db   197 rIleAsnTyrSerGlyAspThrTyrTyrAsnProSerLeuLysSer 212
```

Search completed: August 4, 2005, 18:20:08
Job time : 85.75 secs

```
RESULT 15
Q65ZI1
ID   Q65ZI1          PRELIMINARY;      PRT;   262 AA.
AC   Q65ZI1;
```

```
                    GenCore version 5.1.6
             Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     August 4, 2005, 18:21:34 ; Search time 90 Seconds
                                       (without alignments)
                                       721.953 Million cell updates/sec

Title:           NOLAN463-2A.SEQ
Perfect score:   148
Sequence:        1 ATCATCTATCCTGGTGACTC.........GTATTAGCAGCTGGTTAGCC 84

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.1
                 Ygapop 10.0 , Ygapext  0.1
                 Fgapop  6.0 , Fgapext  0.1
                 Delop   6.0 , Delext   0.1

Searched:        2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters:      4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123943_22574/app_query.fasta_1.5
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-USER=NOLAN08728463-2 @CGN_1_1_308 @runat_04082005_123943_22574 -NCPU=6
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :  A_Geneseq_16Dec04:*
            1: geneseqp1980s:*
            2: geneseqp1990s:*
            3: geneseqp2000s:*
            4: geneseqp2001s:*
            5: geneseqp2002s:*
            6: geneseqp2003as:*
            7: geneseqp2003bs:*
            8: geneseqp2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	114.1	77.1	240	3	AAY15128	Aay15128 Anti-muri
2	104.9	70.9	302	4	AAB70844	Aab70844 SNV-env 1
3	97.9	66.1	116	5	AAM48005	Aam48005 Human mon
4	97.9	66.1	116	8	ADR46821	Adr46821 Human ant
5	97.9	66.1	411	8	ADR46829	Adr46829 Human ant
6	97.9	66.1	468	8	ADR46819	Adr46819 Human ant
7	97.9	66.1	613	8	ADR46827	Adr46827 Human bet
8	96.2	65.0	118	7	ADP47114	Adp47114 Human pho
9	95.4	64.5	129	7	ADK18605	Adk18605 Anti-huma
10	95.4	64.5	129	7	ADK18791	Adk18791 Anti-huma
11	95.4	64.5	129	7	ADK18895	Anti-huma
12	95.4	64.5	129	7	ADK18826	Anti-huma
13	95.4	64.5	129	8	ADL25428	Human mAb
14	94.9	64.1	116	8	ADP22194	Human ant
15	93.8	63.4	118	8	ADP47088	Human pho
16	93.5	63.2	118	8	ADP47090	Human pho
17	93.5	63.2	118	8	ADP47098	Human pho
18	93.5	63.2	245	4	ADP47224	Human pho
19	93.5	63.2	245	4	AAB67621	Human leu
20	93.2	63.0	123	5	ABG76561	HCV E1 an
21	92.4	62.4	225	5	ABR01521	Human ant
22	92.2	62.3	84	4	AAW62797	Amino aci
23	92.2	62.3	98	5	ABG78233	Human Fv
24	92.2	62.3	98	5	ABG78231	Human Fv
25	92.2	62.3	98	5	ABG91924	Human ant
26	92.2	62.3	98	6	ABG91922	Human ant
27	92.2	62.3	98	6	ABP56508	Human ant
28	92.2	62.3	98	6	ABJ18687	Antibody
29	92.2	62.3	98	6	ABO27112	Human ger
30	92.2	62.3	98	7	ADD69247	Human hea
31	92.2	62.3	98	7	ADF10156	Antibody
32	92.2	62.3	98	7	ADF09948	Antibody
33	92.2	62.3	98	7	ADF10053	VEGF anti
34	92.2	62.3	98	7	ADK18943	Anti-huma
35	92.2	62.3	98	7	ADK18888	Anti-huma
36	92.2	62.3	98	7	ADK18877	Anti-huma
37	92.2	62.3	98	7	ADK18878	Anti-huma
38	92.2	62.3	98	7	ADK18912	Anti-huma
39	92.2	62.3	98	7	ADK18582	Anti-huma
40	92.2	62.3	98	7	ADK18890	Anti-huma
41	92.2	62.3	98	7	ADK18896	Anti-huma
42	92.2	62.3	98	7	ADK18894	Anti-huma
43	92.2	62.3	98	7	ADK18914	Anti-huma
44	92.2	62.3	98	7	ADJ80328	VH gene 1
45	92.2	62.3	98	8	ADR46847	Human VH5

ALIGNMENTS

```
RESULT 1
AAY15128
ID   AAY15128 standard; protein; 240 AA.
XX
AC   AAY15128;
XX
DT   07-FEB-2000  (first entry)
XX
DE   Anti-murine CTLA-4 M24 sFv.
XX
KW   Anti-murine CTLA-4 sFv; M24 sFv; single chain antibody; murine CTLA4;
KW   membrane-associated protein; chimeric construct; extracellular domain;
KW   human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;
KW   recipient CD28; T-cell proliferation;
KW   xenograft-specific immunosuppression.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 153
FT                   /note= "Corresponds to atc codon"
XX
PN   WO9957266-A2.
XX
PD   11-NOV-1999.
XX
PF   30-APR-1999;  99WO-GB001350.
XX
PR   30-APR-1998;  98GB-00009280.
XX
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI   Lechler-IR, Dorling A;
```

```
XX
DR   WPI; 2000-038815/03.
DR   N-PSDB; AAZ29000.
XX
PT   Inhibiting T-cell mediated rejection of xenotransplanted organs.
XX
PS   Claim 9; Fig 11; 43pp; English.
XX
CC   The present sequence is the anti-murine CTLA-4 sFv (M24 sFv). This is a
CC   membrane-associated protein which binds to CTLA-4. Chimeric constructs
CC   comprising DNA sequences encoding the extracellular domain of murine
CC   CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.
CC   The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated
CC   T-cells and antagonises the co-stimulatory signal provided by the
CC   interaction between donor B7 and recipient CD28. Cells expressing the
CC   anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in
CC   xenograft-specific immunosuppression
XX
SQ   Sequence 240 AA;

Alignment Scores:
Pred. No.:                0.000165         Length:            240
Score:                     114.10          Matches:            26
Percent Similarity:        23.08%          Conservative:        1
Best Local Similarity:     22.22%          Mismatches:          1
Query Match:               77.09%          Indels:             89
DB:                            3           Gaps:                1

NOLAN463-2A.SEQ (1-84) x AAY15128 (1-240)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC----------- 51
           |||||||||||||||||||||||||||| |||||||||
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy   51 ----------- 51
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89

Qy   51 ----------- 51
Db   90 AspThrAlaValTyrTyrCysAlaAargPheSerLeuGlyGlyPheAspTyrTrpGlyGln 109

Qy   51 ----------- 51
Db  110 GlyThrLeuValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGly 129

Qy   51 ----------- 51
Db  130 SerAlaLeuAspIleGlnLeuThrGlnSerProSerLeuSerAlaSerValGlyAsp 149

Qy   52 CGGGCCAGTCAGGGTATTAGCAGCTGGTTAGCC 84
           |||||      :::||||||
Db  150 ArgValThrThrCysArgAlaSerGlnGlyIleSerSerSerTyrLeuAla 166

RESULT 2
AAB70844
ID   AAB70844 standard; protein; 302 AA.
XX
AC   AAB70844;
XX
DT   11-SEP-2003 (revised)
DT   25-JUN-2001 (first entry)
XX
DE   SNV-env leader/human 6C3-scFv fusion construct.
XX
KW   T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW   cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW   gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW   acquired immune deficiency syndrome; severe combined immune deficiency;
KW   T cell lymphoma; fusion construct.
XX
OS   Homo sapiens.
OS   Spleen necrosis virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..45
FT                   /label= SNV-env_leader
FT   Protein         46..302
FT                   /label= 6C3-scFv
XX
PN   DEI9946142-A1.
XX
PD   29-MAR-2001.
XX
PF   27-SEP-1999;  99DE-01046142.
XX
PR   27-SEP-1999;  99DE-01046142.
XX
PA   (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
PI   Cichutek K, Engelstaedter M;
XX
DR   WPI; 2001-246140/26.
DR   N-PSDB; AAF61513.
XX
PT   Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT   of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT   variable antibody fragment.
XX
PS   Claim 1; Fig 5; 18pp; German.
XX
CC   This invention describes a novel cell-targeting vector (A) containing a
CC   DNA sequence (I) encoding a single-chain variable antibody fragment
CC   (scFv). The products of the invention have antiviral, cytostatic and
CC   immunostimulant activity and can be used in gene therapy, immunization
CC   and diagnosis particularly of T cell-associated diseases, specifically
CC   acquired immune deficiency syndrome (AIDS), severe combined immune
CC   deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC   of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC   human B cells, and 1000 fold selectivity over other human cells. A vector
CC   designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC   fragment, fully defined in the specification. It was used to transform
CC   D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC   (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC   carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC   determine transformation. The viral titer (infectious units/ml) was over
CC   1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC   showing the high selectivity for human T cells. This sequence represents
CC   the SNV-env leader/human 6C3-scFv fusion construct used in the
CC   construction of novel cell targeting vectors described in the invention.
CC   (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 302 AA;

Alignment Scores:
Pred. No.:                0.00218          Length:            302
Score:                     104.90          Matches:            23
Percent Similarity:        19.38%          Conservative:        2
Best Local Similarity:     17.83%          Mismatches:          3
Query Match:               70.88%          Indels:            101
DB:                            4           Gaps:                1

NOLAN463-2A.SEQ (1-84) x AAB70844 (1-302)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC----------- 51
           ::||||||||||||||||||| ||||||||||||||||
Db   97 LeuIleTyrProGlyAspSerAspThrLysTyrSerProSerPheGlnGlyGlnValThr 116

Qy   51 ----------- 51
Db  117 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 136

Qy   51 ----------- 51
Db  137 AspThrAlaMetTyrTyrCysAlaAargValSerGlyTyrCysSerSerThrSerCysTyr 156
```

```
Qy    51 -------------------------------------------------- 51
Db   157 AspTyrTyrTyrTyrMetAspValTrpGlyArgGlyArgThrLeuValThrValSerArg 176

Qy    51 -------------------------------------------------- 51
Db   177 GlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlySerGlyGlySerAspIleValMetThr 196

Qy    52 --------------------------------------------CGGGCG 57
                                                     |||||
Db   197 GlnSerProSerThrLeuSerAlaSerValGlyAspArgValThrMetThrCysArgAla 216

Qy    58 AGTCAGGGTATTAGCAGCTGGTTAGCC 84
         ||||||  |||:::  |||||||
Db   217 SerGlnAsnIleAsnIleTrpLeuAla 225
```

RESULT 3
AAM48005
ID   AAM48005 standard; protein; 116 AA.
XX
AC   AAM48005;
XX
DT   08-MAR-2002 (first entry)
XX
DE   Human monoclonal antibody B11 variable heavy chain protein.
XX
KW   Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
KW   mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
KW   autoimmune disease; inflammatory disorder; rheumatoid arthritis;
KW   multiple sclerosis; diabetes mellitus; immunomodulatory;
KW   antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
KW   antidiabetic; antianaemic; endocrine; dermatological; antithyroid;
KW   uropathic; ophthalmological; muscular.
XX
OS   Homo sapiens.
XX
PN   WO200185798-A2.
XX
PD   15-NOV-2001.
XX
PF   08-MAY-2001; 2001WO-US015114.
XX
PR   08-MAY-2000; 2000US-0203126P.
PR   07-SEP-2000; 2000US-0230739P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Deo YM, Keler T;
XX
DR   WPI; 2002-089788/12.
DR   N-PSDB; ABA05500.
XX
PT   New human monoclonal antibodies specific for dendritic cells, useful for
PT   inhibiting growth or inducing cytolysis of a dendritic cell and treating
PT   or preventing a dendritic cell mediated disease, e.g., autoimmune
PT   disorders.
XX
PS   Example 2; Fig 13; 95pp; English.
XX
CC   The invention relates to human monoclonal antibodies or their antigen
CC   binding portions that specifically bind to dendritic cells and has one or
CC   more of the following characteristics: (a) a binding affinity constant to
CC   a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability
CC   to opsonise a dendritic cell; (c) the ability to internalise after
CC   binding to dendritic cells; or (d) the ability to activate dendritic
CC   cells. The isolated human monoclonal antibody or its antigen binding
CC   portion may also have any of the following characteristics: (a) mediates
CC   cytolysis of dendritic cells in the presence of human effector cells; or
CC   (b) inhibits growth of dendritic cells. The antibodies or its antigen
CC   binding portion, binds to and blocks the human mannose receptor on
CC   dendritic cells. The antibodies have immunomodulatory, antiinflammatory,
CC   antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianaemic,

CC   endocrine, dermatological, antithyroid, uropathic, ophthalmological and
CC   muscular activity. The antibodies or their antigen-binding fragments are
CC   useful for inhibiting growth of a dendritic cell, inducing cytolysis of a
CC   dendritic cell, treating or preventing a dendritic cell mediated disease,
CC   detecting the presence of a dendritic cell, targeting an antigen to a
CC   dendritic cell and preventing binding of a pathogen (a virus or a
CC   bacterium) to human mannose receptor on dendritic cells. In particular,
CC   the antibodies may be used to treat, autoimmune disease, graft versus
CC   host disease, immune system or inflammatory disorders (e.g. rheumatoid
CC   arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,
CC   pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's
CC   syndrome and Graves disease. The present sequence is that of the human
CC   monoclonal antibody B11 variable heavy chain, useful to the invention
XX
SQ   Sequence 116 AA;

Alignment Scores:
Pred. No.:   0.0111   Length: 116
Score: 97.90   Matches: 19
Percent Similarity: 36.84%   Conservative: 2
Best Local Similarity: 33.33%   Mismatches: 5
Query Match: 66.15%   Indels: 31
DB: 5   Gaps: 1

NOLAN463-2A.SEQ (1-84) x AAM48005 (1-116)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC---------- 51
         |||||||||||||||||||||||||| |||||||||||
Db   50 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyValThr 69

Qy   51 -- 51
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89

Qy   52 -------------------------CGGGCGAGTCAGGGTATTAGCAGCTGG 78
                                  || ::||||:::
Db   90 AspThrAlaMetTyrTyrCysThrArgArgGlyValAspArgGlyTyrTrp 106

RESULT 4
ADR46821
ID   ADR46821 standard; protein; 116 AA.
XX
AC   ADR46821;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
XX
KW   molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW   antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW   betahCG; beta chorionic gonadotropin; antibody;
KW   T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW   immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW   CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW   melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW   antibody B11; heavy chain variable region.
XX
OS   Homo sapiens.
XX
PN   WO2004074432-A2.
XX
PD   02-SEP-2004.
XX
PF   30-JAN-2004; 2004WO-US002725.
XX
PR   31-JAN-2003; 2003US-0443979P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T, Endres M, He L, Ramakrishna V;
XX
DR   WPI; 2004-635555/61.
DR   N-PSDB; ADR46820.

XX
PT New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT cytotoxic T cell response in cancers and infectious diseases.
XX
PS Claim 11; SEQ ID NO 4; 82pp; English.
XX
CC The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADR46829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates
CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human antibody B11 heavy chain
CC variable region, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 116 AA;

Alignment Scores:
Pred. No.: 0.0111 Length: 116
Score: 97.90 Matches: 19
Percent Similarity: 36.84% Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match: 66.15% Indels: 31
DB: 8 Gaps: 1

NOLAN463-2A.SEQ (1-84) x ADR46821 (1-116)

Qy 1 ATCATCTATCCTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC---------- 51
        |||||||||||||||||||||| ||||||||||
Db 50 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 69

Qy 51 -- 51

Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89

Qy 52 ----------CGGGCGAGTCAGGGTATTAGCAGTCGG 78
           ||| :::||||:: |||
Db 90 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106

RESULT 5
ADR46829
ID   ADR46829 standard; protein; 411 AA.
XX

AC ADR46829;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.
XX
KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; pB11-betahCG molecular conjugate; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200074432-A2.
XX
PD 02-SEP-2004.
XX
PF 30-JAN-2004; 2004WO-US002725.
XX
PR 31-JAN-2003; 2003US-0443979P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Keler T, Endres M, He L, Ramakrishna V;
XX
DR WPI; 2004-635555/61.
DR N-PSDB; ADR46828.
XX
PT New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT cytotoxic T cell response in cancers and infectious diseases.
XX
PS Claim 16; SEQ ID NO 12; 82pp; English.
XX
CC The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADR46829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates
CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and

CC   herpes. The present sequence represents a human pB11-betahCG molecular
CC   conjugate, which is used in the exemplification of the present invention.
XX
SQ   Sequence 411 AA;

Alignment Scores:
Pred. No.:   0.0162   Length: 411
Score: 97.90   Matches: 19
Percent Similarity: 36.84%   Conservative: 2
Best Local Similarity: 33.33%   Mismatches: 5
Query Match: 66.15%   Indels: 31
DB: Gaps: 8

NOLAN463-2A.SEQ (1-84) x ADR46829 (1-411)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGC--------- 51
          ||||||||||||||||||||||||||||||||| |||||||
Db   191 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 210

Qy   51 --- 51

Db   211 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 230

Qy   52 ---------------------------------CGGGCGAGTCAGGGTATTAGCAGCTGG 78
                                           ||| :::||||::: |||
Db   231 AspThrAlaMetTyrTyrCysThrArgGlyValAspArgGlyValAspTyrTyrTrp 247

RESULT 6
ADR46819
ID   ADR46819 standard; protein; 468 AA.
XX
AC   ADR46819;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human antibody B11 heavy chain variable region protein SEQ ID NO:2.
XX
KW   molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW   antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW   betahCG; beta chorionic gonadotropin; antibody;
KW   T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW   immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW   CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW   melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW   antibody B11; heavy chain variable region.
XX
OS   Homo sapiens.
XX
PN   WO200074432-A2.
XX
PD   02-SEP-2004.
XX
PF   30-JAN-2004; 2004WO-US002725.
XX
PR   31-JAN-2003; 2003US-0443979P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T, Endres M, He L, Ramakrishna V;
XX
DR   WPI; 2004-635555/61.
DR   N-PSDB; ADR46818.
XX
PT   New molecular conjugate having a monoclonal antibody that binds to human
PT   APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT   cytotoxic T cell response in cancers and infectious diseases.
XX
PS   Claim 13; SEQ ID NO 2; 82pp; English.
XX
CC   The present invention describes a molecular conjugate comprising a
CC   monoclonal antibody that binds to human antigen presenting cells (APCs)
CC   linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC   comprises a heavy and/or light chain variable region derived from a human

CC   VH5-51 or Vk-ft5 germline sequence with the 98 or 95 amino acid sequences
CC   of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC   described: a molecular conjugate comprising a human antibody heavy
CC   chain and a human antibody light chain, where either or both chains are
CC   linked to betahCG; (2) a molecular conjugate comprising a human single
CC   chain antibody that binds to human APCs linked to betahCG, where the
CC   conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC   (ADR46829); (3) a composition comprising any of the molecular conjugates
CC   as described above, and a carrier, optionally in combination with an
CC   adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC   against betahCG, comprising contacting any of the molecular conjugates
CC   described above with APCs such that the antigen is processed and
CC   presented to T cells in a manner which induces or enhances a T cell-
CC   mediated response against the antigen; (5) immunising a subject
CC   comprising administering any of the molecular conjugates described above,
CC   optionally in combination with an adjuvant, a cytokine which stimulates
CC   proliferation of dendritic cells and/or an immunostimulatory agent; and
CC   (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC   comprising forming a conjugate of the antigen and a monoclonal antibody
CC   which binds to APCs, and contacting the conjugate either in vivo or ex
CC   vivo with APCs such that the antigen is internalised, processed and
CC   presented to T cells in a manner which induces or enhances a cytotoxic T
CC   cell response against the antigen. The molecular conjugate has
CC   cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC   virucide and antimalarial activities, and can be used as a CD8 agonist,
CC   and in vaccines. The methods and compositions of the present invention
CC   are useful for inducing a cytotoxic T cell response, and in particular
CC   for treating autoimmune disorders, cancers and infectious diseases by
CC   eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC   including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC   herpes. The present sequence represents a human antibody B11 heavy chain
CC   variable region, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 468 AA;

Alignment Scores:
Pred. No.:   0.0168   Length: 468
Score: 97.90   Matches: 19
Percent Similarity: 36.84%   Conservative: 2
Best Local Similarity: 33.33%   Mismatches: 5
Query Match: 66.15%   Indels: 31
DB: Gaps: 8

NOLAN463-2A.SEQ (1-84) x ADR46819 (1-468)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGC--------- 51
          ||||||||||||||||||||||||||||||||| |||||||
Db   69 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 88

Qy   51 --- 51

Db   89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108

Qy   52 ---------------------------------CGGGCGAGTCAGGGTATTAGCAGCTGG 78
                                           ||| :::||||::: |||
Db   109 AspThrAlaMetTyrTyrCysThrArgGlyValAspArgGlyValAspTyrTyrTrp 125

RESULT 7
ADR46827
ID   ADR46827 standard; protein; 613 AA.
XX
AC   ADR46827;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.
XX
KW   molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW   antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW   betahCG; beta chorionic gonadotropin; antibody;
KW   T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW   immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;

```
DB:                                    8          Gaps:        1

NOLAN463-2A.SEQ (1-84) x ADR46827 (1-613)

Qy     1 ATCATCATCCTGTGACTCTGATACCACATACAGCCGTCCTTCCAAGGC------- 51
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db    69 IleIleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 88

Qy    51 ------------------------------------------------------ 51

Db    89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108

Qy    52 -----------------------CGGGCGAGTCAGGTATTAGCAGCTGG 78
                                 ||| :::||||.:::
Db   109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125
```

RESULT 8
ADP47114
ID ADP47114 standard; protein; 118 AA.
XX
AC ADP47114;
XX
DT 09-SEP-2004 (first entry)
DE Human phospholipase A2-specific monoclonal antibody heavy chain #14.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction: skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L,   Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Claim 1; SEQ ID NO 29; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents the heavy chain from a monoclonal antibody
CC that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
SQ Sequence 118 AA;

Alignment Scores:
Pred. No.:   0.0178   Length: 118
Score: 96.20   Matches: 21
Percent Similarity: 67.65%   Conservative: 2
Best Local Similarity: 61.76%   Mismatches: 3
Query Match: 65.00%   Indels: 8
```

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```
KW  CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW  melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW  antibody B11; betahCG-B11 molecular conjugate; fusion protein.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO2004074432-A2.
XX
PD  02-SEP-2004.
XX
PF  30-JAN-2004; 2004WO-US002725.
XX
PR  31-JAN-2003; 2003US-0443979P.
XX
PA  (MEDA-) MEDAREX INC.
XX
PI  Keler T,  Endres M,  He L,  Ramakrishna V;
XX
DR  WPI; 2004-635555/61.
DR  N-PSDB; ADR46826.
XX
PT  New molecular conjugate having a monoclonal antibody that binds to human
PT  APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT  cytotoxic T cell response in cancers and infectious diseases.
XX
PS  Example 1; SEQ ID NO 10; 82pp; English.
XX
CC  The present invention describes a molecular conjugate comprising a
CC  monoclonal antibody that binds to human antigen presenting cells (APCs)
CC  linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC  comprises a heavy and/or light chain variable region derived from a human
CC  VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC  of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC  described: (1) a molecular conjugate comprising a human antibody heavy
CC  chain and a human antibody light chain, where either or both chains are
CC  linked to betahCG; (2) a molecular conjugate comprising a human single
CC  chain antibody that binds to human APCs linked to betahCG, where the
CC  conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC  (ADR46829); (3) a composition comprising any of the molecular conjugates
CC  as described above, and a carrier, optionally in combination with an
CC  adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC  against betahCG, comprising contacting any of the molecular conjugates
CC  described above with APCs such that the antigen is processed and
CC  presented to T cells in a manner which induces or enhances a T cell-
CC  mediated response against the antigen; (5) immunising a subject
CC  comprising administering any of the molecular conjugates described above,
CC  optionally in combination with an adjuvant, a cytokine which stimulates
CC  proliferation of dendritic cells and/or an immunostimulatory agent; and
CC  (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC  comprising forming a conjugate of the antigen and a monoclonal antibody
CC  which binds to APCs, and contacting the conjugate either in vivo or ex
CC  vivo with APCs such that the antigen is internalised, processed and
CC  presented to T cells in a manner which induces or enhances a cytotoxic T
CC  cell response against the antigen. The molecular conjugate has
CC  cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC  virucide and antimalarial activities, and can be used as a CD8 agonist,
CC  and in vaccines. The methods and compositions of the present invention
CC  are useful for inducing a cytotoxic T cell response, and in particular
CC  for treating autoimmune disorders, cancers and infectious diseases by
CC  eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC  including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC  herpes. The present sequence represents a human betahCG-B11 molecular
CC  conjugate, which is used in the exemplification of the present invention.
XX
SQ  Sequence 613 AA;

Alignment Scores:
Pred. No.:                          0.0182        Length:             613
Score:                              97.90         Matches:             19
Percent Similarity:                 36.84%        Conservative:         2
Best Local Similarity:              33.33%        Mismatches:           5
Query Match:                        66.15%        Indels:              31
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```
DB:                     8               Gaps:          2

NOLAN463-2A.SEQ (1-84) x ADP47114 (1-118)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db  50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy  55 -----GCGAGTCAGGGTATTAGCAGC-----------TGG 78
             ||| ||| ||||||:::
Db  70 IleSerAlaAspGlnSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 9
ADK18605
ID   ADK18605 standard; protein; 129 AA.
XX
AC   ADK18605;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Anti-human PDGF-D antibody heavy chain protein sequence.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 29; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 3064188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 129 AA;

Alignment Scores:
Pred. No.:             0.0228         Length:          129
Score:                 95.40          Matches:         20
Percent Similarity:    57.50%         Conservative:    3
Best Local Similarity: 50.00%         Mismatches:      16
Query Match:           64.46%         Indels:          1
DB:                                   Gaps:            7

Sequence 129 AA;

NOLAN463-2A.SEQ (1-84) x ADK18605 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
        |||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db  50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69
```

```
Qy  61 CAGGGTATTAGCAGC---------------------TGG 78
        |||||:::
Db  70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 10
ADK18791
ID   ADK18791 standard; protein; 129 AA.
XX
AC   ADK18791;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #17.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 215; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 3064188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 129 AA;

Alignment Scores:
Pred. No.:             0.0228         Length:          129
Score:                 95.40          Matches:         20
Percent Similarity:    57.50%         Conservative:    3
Best Local Similarity: 50.00%         Mismatches:      1
Query Match:           64.46%         Indels:          16
DB:                                   Gaps:            1

Sequence 129 AA;

NOLAN463-2A.SEQ (1-84) x ADK18791 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
        |||||||||||||||||||||||||||||  |||||||||||||||||||:::
Db  50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69

Qy  61 CAGGGTATTAGCAGC---------------------TGG 78
        |||||:::
Db  70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 11
ADK18895
```

ID   ADK18895 standard; protein; 129 AA.
XX
AC   ADK18895;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #121.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200305785785-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 319; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 3066418.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-3066418. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 129 AA;

Alignment Scores:
Pred. No.:   0.0228   Length: 129
Score: 95.40   Matches: 20
Percent Similarity: 57.50%   Conservative: 3
Best Local Similarity: 50.00%   Mismatches: 1
Query Match: 64.46%   Indels: 16
DB: Gaps: 7

NOLAN463-2A.SEQ (1-84) x ADK18895 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
             ||||||||||||||||||||||||||||||||| ||||||||||||||||:::||||||
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69

Qy   61 CAGGGTATTAGCAGC------------------------------TGG 78
             ||||||::: |||
Db   70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 12
ADK18826
ID   ADK18826 standard; protein; 129 AA.
XX
AC   ADK18826;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #52.

ID   ADK18895 standard; protein; 129 AA.
XX
AC   ADK18895;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #121.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200305785785-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 250; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 3066418.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-3066418. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 129 AA;

Alignment Scores:
Pred. No.:   0.0228   Length: 129
Score: 95.40   Matches: 20
Percent Similarity: 57.50%   Conservative: 3
Best Local Similarity: 50.00%   Mismatches: 1
Query Match: 64.46%   Indels: 16
DB: Gaps: 7

NOLAN463-2A.SEQ (1-84) x ADK18826 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
             |||||||||||||||||||||||||||||||||||||||||||:::||||||
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69

Qy   61 CAGGGTATTAGCAGC------------------------------TGG 78
             ||||||::: |||
Db   70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 13
ADL25428
ID   ADL25428 standard; protein; 129 AA.
XX
AC   ADL25428;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Human mAb 1.29 heavy chain variable region protein SEQ ID NO:38.
XX
KW   antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW   nephritis; mesangial cell proliferation inhibition;
KW   mesangial proliferative glomerulonephritis; nephrotropic;
KW   antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW   gene therapy; human; monoclonal antibody; mAb.
XX

```
OS   Homo sapiens.
XX
PN   WO2004024098-A2.
XX
PD   25-MAR-2004.
XX
DR   WPI; 2004-269881/25.
DR   N-PSDB; ADL25427.
XX
PI   Floege J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;
XX
PA   (ABGE-) ABGENIX INC.
PA   (CURA-) CURAGEN CORP.
XX
PT   Use of an antibody or its binding fragment that binds platelet derived
PT   growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT   nephritis.
XX
PS   Disclosure; SEQ ID NO 38; 115pp; English.
XX
CC   The present invention describes an antibody or its binding fragment that
CC   binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC   useful in preparing a medicament for treating nephritis. Also described:
CC   (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC   (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC   of treating mesangial proliferative glomerulonephritis. The antibody has
CC   nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC   antidiabetic activities, and can be used in gene therapy. The antibody or
CC   its binding fragment, that binds PDGF-DD, can be used in preparing a
CC   medicament for treating nephritis and related disorders, e.g. mesangial
CC   proliferative glomerulonephritis. The present sequence represents a human
CC   monoclonal antibody (mAb) variable region sequence, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 129 AA;

Alignment Scores:
Pred. No.:              0.0228          Length:            129
Score:                  95.40           Matches:           20
Percent Similarity:     57.50%          Conservative:       3
Best Local Similarity:  50.00%          Mismatches:         1
Query Match:            64.46%          Indels:            16
DB:                                     Gaps:               8

NOLAN463-2A.SEQ (1-84) x ADL25428 (1-129)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCATACAGCCCGTCCTTCCAAGGCGGGCCAGT   60
         ||||||||||||||||||||||||||||||  |||||||||||||||::||||||
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr  69

Qy   61 CAGGGTATTAGCAGC-----------------------------TGG   78
         |||||:::                                     |||
Db   70 -----IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp   83

RESULT 14
ADP22194
ID   ADP22194 standard; protein; 116 AA.
XX
AC   ADP22194;
XX
DT   09-SEP-2004 (first entry)
XX
DE   Human anti-TNFa antibody light chain variable region  SEQ ID NO:100.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200405683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI   Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI   Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
DR   N-PSDB; ADP22193.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 100; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence represents a human anti-TNFa
CC   antibody light chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 116 AA;

Alignment Scores:
Pred. No.:              0.0253          Length:            116
Score:                  94.90           Matches:           19
Percent Similarity:     36.84%          Conservative:       2
Best Local Similarity:  33.33%          Mismatches:         5
Query Match:            64.12%          Indels:            31
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```
DB:                        8                    Gaps:        1

NOLAN463-2A.SEQ (1-84) x ADP22194 (1-116)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC---------  51
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyValThr     69

Qy   51 -------------                                                 51
Db   70 IleSerAlaAspLysSerIleThrThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer  89

Qy   52 --------------CGGGCGAGTCAGGGTATTAGCAGCTGG                      78
                      ||||:::  |||||||   |||
Db   90 AspThrAlaMetTyrTyrCysAlaArgSerGlyTyrGlyMetAspValTrp          106
```

```
DB:                        8                    Gaps:        1

NOLAN463-2A.SEQ (1-84) x ADP47088 (1-118)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCG---  57
        |||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db    1 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr  69

Qy   57 -------------                                                 57
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer  89

Qy   58 -----------------AGTCAGGGTATTAGCAGCTGG                        78
                         |||  |||:::   |||
Db   90 AspThrAlaMetTyrTyrCysAlaArgHisTrpSerTyrGlyMetAspValTrp       107
```

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Search completed: August  4,  2005, 18:55:54
Job time : 96 secs
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```
RESULT 15
ADP47088
ID   ADP47088 standard; protein; 118 AA.
XX
AC   ADP47088;
XX
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human phospholipase A2-specific monoclonal antibody heavy chain #1.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS   Homo sapiens.
XX
XX
PN   WO2004050850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038234.
XX
PR   02-DEC-2002; 2002US-0430724P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Landes GM, Haak-Frendscho M, Chen L,  Lee YR,  Liang ML,  Feng X;
PI   Jia X, Nocerini MR;
XX
DR   WPI; 2004-461119/43.
XX
PT   New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT   useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT   asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS   Claim 1; SEQ ID NO 3; 128pp; English.
XX
CC   The invention comprises a human monoclonal antibody that binds to
CC   phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC   useful in the preparation of a medicament for the treatment of
CC   inflammatory and degenerative disorders stemming from inflammatory
CC   reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC   asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC   amino acid sequence represents the heavy chain from a monoclonal antibody
CC   that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
SQ   Sequence 118 AA;

Alignment Scores:
Pred. No.:              0.0343
Score:                  93.80              Length:         118
Percent Similarity:     36.21%             Matches:         19
Best Local Similarity:  32.76%             Conservative:     2
Query Match:            63.38%             Mismatches:       5
                                           Indels:          32
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OM nucleic - protein search, using frame_plus_n2p model

                 GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:   August 4, 2005, 18:44:26 ; Search time 22.25 Seconds
                                     (without alignments)
                                     563.642 Million cell updates/sec

Title:          NOLAN463-2A.SEQ
Perfect score:  148
Sequence:       1 ATCATCTATCCTGGTGACTC.........GTATTAGCAGCTCGGTTAGCC 84

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                Ygapop 10.0 , Ygapext  0.1
                Fgapop  6.0 , Fgapext  0.1
                Delop   6.0 , Delext   0.1

Searched:       513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:        1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN_1_1.66 @runat_04082005 123945_22604 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

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        6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match *	Length	DB	ID	Description
1	92.2	62.3	98	2	US-08-665-202-33	Sequence 33, Appl
2	92.2	62.3	98	4	US-09-315-574-33	Sequence 33, Appl
3	92.2	62.3	111	4	US-09-726-219A-171	Sequence 171, App
4	92.2	62.3	117	3	US-08-545-809A-133	Sequence 133, Appl
5	92.2	62.3	119	3	US-09-025-769B-26	Sequence 26, Appl
6	92.2	62.3	119	4	US-09-490-070A-26	Sequence 26, Appl
7	92.2	62.3	119	4	US-09-490-153-26	Sequence 26, Appl
8	92.2	62.3	119	4	US-09-490-324-26	Sequence 26, Appl
9	92.2	62.3	120	3	US-09-025-769B-40	Sequence 40, Appl
10	92.2	62.3	120	3	US-09-025-769B-67	Sequence 67, Appl
11	92.2	62.3	120	4	US-09-490-070A-40	Sequence 40, Appl
12	92.2	62.3	120	4	US-09-490-070A-67	Sequence 67, Appl
13	92.2	62.3	120	4	US-09-490-153-40	Sequence 40, Appl
14	92.2	62.3	120	4	US-09-490-153-67	Sequence 67, Appl
15	92.2	62.3	120	4	US-09-490-324-40	Sequence 40, Appl
16	92.2	62.3	120	4	US-09-490-324-67	Sequence 67, Appl
17	91.2	61.6	98	1	US-08-478-039-81	Sequence 81, Appl
18	91.2	61.6	98	1	US-08-476-349A-81	Sequence 81, Appl
19	91.2	61.6	125	2	US-08-665-202-46	Sequence 46, Appl
20	91.2	61.6	125	2	US-08-665-202-53	Sequence 53, Appl
21	91.2	61.6	125	2	US-08-665-202-54	Sequence 54, Appl
22	91.2	61.6	125	4	US-09-315-574-46	Sequence 46, Appl
23	91.2	61.6	125	4	US-09-315-574-53	Sequence 53, Appl
24	91.2	61.6	125	4	US-09-315-574-54	Sequence 54, Appl
25	88.4	59.7	125	2	US-08-665-202-44	Sequence 44, Appl
26	88.4	59.7	125	2	US-08-665-202-45	Sequence 45, Appl
27	88.4	59.7	125	2	US-08-665-202-47	Sequence 47, Appl
28	88.4	59.7	125	2	US-08-665-202-48	Sequence 48, Appl
29	88.4	59.7	125	2	US-08-665-202-49	Sequence 49, Appl
30	88.4	59.7	125	2	US-08-665-202-50	Sequence 50, Appl
31	88.4	59.7	125	2	US-08-665-202-51	Sequence 51, Appl
32	88.4	59.7	125	2	US-08-665-202-52	Sequence 52, Appl
33	88.4	59.7	125	2	US-08-665-202-55	Sequence 55, Appl
34	88.4	59.7	125	2	US-08-665-202-57	Sequence 57, Appl
35	88.4	59.7	125	2	US-08-665-202-58	Sequence 58, Appl
36	88.4	59.7	125	4	US-09-315-574-44	Sequence 44, Appl
37	88.4	59.7	125	4	US-09-315-574-45	Sequence 45, Appl
38	88.4	59.7	125	4	US-09-315-574-47	Sequence 47, Appl
39	88.4	59.7	125	4	US-09-315-574-48	Sequence 48, Appl
40	88.4	59.7	125	4	US-09-315-574-49	Sequence 49, Appl
41	88.4	59.7	125	4	US-09-315-574-50	Sequence 50, Appl
42	88.4	59.7	125	4	US-09-315-574-51	Sequence 51, Appl
43	88.4	59.7	125	4	US-09-315-574-52	Sequence 52, Appl
44	88.4	59.7	125	4	US-09-315-574-55	Sequence 55, Appl
45	88.4	59.7	125	4	US-09-315-574-57	Sequence 57, Appl

ALIGNMENTS

```
RESULT 1
US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
;   APPLICANT: Marks, James D.
;   APPLICANT: Schier, Robert
;   TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
;   TITLE OF INVENTION: Tumor Antigens
;   NUMBER OF SEQUENCES: 141
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/665,202
;     FILING DATE: 13-JUN-1996
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/000,238
;     FILING DATE: 14-JUN-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/000,250
;     FILING DATE: 15-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hunter, Tom
;     REGISTRATION NUMBER: 38,498
;     REFERENCE/DOCKET NUMBER: 02307E-061410
```

;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 98 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-665-202-33

Alignment Scores:
Pred. No.:   0.00843
Score: 92.20
Percent Similarity: 67.65%
Best Local Similarity: 58.82%
Query Match: 62.30%
DB: 2

Length: 98
Matches: 20
Conservative: 3
Mismatches: 3
Indels: 8
Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-08-665-202-33 (1-98)

Qy   1 ATCATCTATCCTGCTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        |||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy 55 ------GCGAGTCAGGGTATTAGCAGC-----------------TGG 78
         ||| ::: ||||||::| ||||||:::
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 2
US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
;   APPLICANT: Marks, James D.
;   APPLICANT: Schier, Robert
;   TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
;   TITLE OF INVENTION: Tumor Antigens
;   NUMBER OF SEQUENCES: 141
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
;   STREET: Four Embarcadero Center, Suite 1100
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-4106
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/315,574
;   FILING DATE: 20-MAY-99
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/000,238
;   FILING DATE: 14-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/000,250
;   FILING DATE: 15-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/665,202
;   FILING DATE: 13-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Hunter, Tom
;   REGISTRATION NUMBER: 38,498
;   REFERENCE/DOCKET NUMBER: 02307E-061411
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:

;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 98 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-315-574-33

Alignment Scores:
Pred. No.:   0.00843
Score: 92.20
Percent Similarity: 67.65%
Best Local Similarity: 58.82%
Query Match: 62.30%
DB: 4

NOLAN463-2A.SEQ (1-84) x US-09-315-574-33 (1-98)

Length: 98
Matches: 20
Conservative: 3
Mismatches: 3
Indels: 8
Gaps: 2

Qy   1 ATCATCTATCCTGCTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        |||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy 55 ------GCGAGTCAGGGTATTAGCAGC-----------------TGG 78
         ||| ::: ||||||::| ||||||:::
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 3
US-09-726-219A-171
; Sequence 171, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
;   APPLICANT: Cambridge Antibody Technology
;   APPLICANT: Cambridge Antibody Technology Limited
;   APPLICANT: Medical Research Council
;   APPLICANT: McCafferty, John
;   APPLICANT: Pope, Anthony
;   APPLICANT: Johnson, Kevin
;   APPLICANT: Hoogenboom, Hendricus
;   APPLICANT: Griffiths, Andrew
;   APPLICANT: Jackson, Ronald
;   APPLICANT: Holliger, Kasper
;   APPLICANT: Marks, James
;   APPLICANT: Clackson, Timothy
;   APPLICANT: Chiswell, David
;   APPLICANT: Winter, Gregory
;   APPLICANT: Bonert, Timothy
;   TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
;   FILE REFERENCE: 213839-00013
;   CURRENT APPLICATION NUMBER: US/09/726,219A
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: GB 9015198.6
;   PRIOR FILING DATE: 1990-07-10
;   PRIOR APPLICATION NUMBER: GB 9022845.3
;   PRIOR FILING DATE: 1990-10-19
;   PRIOR APPLICATION NUMBER: GB 9022845.3
;   PRIOR FILING DATE: 1990-10-19
;   PRIOR APPLICATION NUMBER: GB 9024503.6
;   PRIOR FILING DATE: 1990-11-12
;   PRIOR APPLICATION NUMBER: GB 9104744.9
;   PRIOR FILING DATE: 1991-03-06
;   PRIOR APPLICATION NUMBER: GB 9110549.4
;   PRIOR FILING DATE: 1991-05-15
;   PRIOR APPLICATION NUMBER: PCT/GB91/01134
;   PRIOR FILING DATE: 1991-07-10
;   PRIOR APPLICATION NUMBER: US 07/971,857
;   PRIOR FILING DATE: 1993-01-08
;   PRIOR APPLICATION NUMBER: US 08/484,893
;   PRIOR FILING DATE: 1995-06-07
;   NUMBER OF SEQ ID NOS: 272
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
;   LENGTH: 111
;   TYPE: PRT

; ORGANISM: Homo sapiens
US-09-726-219A-171

Alignment Scores:
Pred. No.:   0.00879
Score: 92.20
Percent Similarity: 67.65%
Best Local Similarity: 58.82%
Query Match: 62.30%
DB:

Length: 111
Matches: 20
Conservative: 3
Mismatches: 3
Indels: 8
Gaps: 2

US-08-545-809A-133

NOLAN463-2A.SEQ (1-84) x US-09-726-219A-171 (1-111)

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Qy    1 ATCACTCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy   55 ------GCGAGTCAGGGTATTAGCAGC----------TGG 78
              ||| :: ||||||:::||
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuHisTrp 83
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RESULT 4
US-08-545-809A-133
; Sequence 133, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT: Honjo, Tasuku
;   APPLICANT: Matsuda, Fumihiko
;   TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES: 145
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: US
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/545,809A
;   FILING DATE: 27-MAR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP93/00603
;   FILING DATE: 10-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Freeman, John W.
;   REGISTRATION NUMBER: 29,066
;   REFERENCE/DOCKET NUMBER: 06501/004001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-542-5070
;   TELEFAX: 617-542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 133:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-545-809A-133

Alignment Scores:
Pred. No.:   0.00895
Score: 92.20
Percent Similarity: 67.65%
Best Local Similarity: 58.82%
Query Match: 62.30%
DB:

Length: 117
Matches: 20
Conservative: 3
Mismatches: 3
Indels: 8
Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-08-545-809A-133 (1-117)

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Qy    1 ATCACTCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   69 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 88

Qy   55 ------GCGAGTCAGGGTATTAGCAGC----------TGG 78
              ||| :: ||||||:::||
Db   89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 102
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RESULT 5
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   APPLICANT: Pack, Peter
;   APPLICANT: Ilag, Vic
;   APPLICANT: Ge, Liming
;   APPLICANT: Moroney, Simon
;   APPLICANT: Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10021
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769B
;   FILING DATE: 18-FEB-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9000
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-025-769B-26

Alignment Scores:
Pred. No.:   0.009
Score: 92.20
Percent Similarity: 67.65%
Best Local Similarity: 58.82%
Query Match: 62.30%
DB:

Length: 119
Matches: 20
Conservative: 3
Mismatches: 3
Indels: 8
Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-025-769B-26 (1-119)

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Qy    1 ATCACTCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy   55 ------GCGAGTCAGGGTATTAGCAGC----------TGG 78
              ||| :: |||
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Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 6
US-09-490-070A-26
; Sequence 26, Application US/09490070A
Patent No. 6696248
  GENERAL INFORMATION:
    APPLICANT: Knappik, Achim
              Pack, Peter
              Ilag, Vic
              Ge, Liming
              Moroney, Simon
              Plueckthun, Andreas
  TITLE OF INVENTION: Protein/(Poly)peptide libraries
  NUMBER OF SEQUENCES: 373
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
              White & McAuliffe
    STREET: 1666 K Street, N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20006
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/490,070A
    FILING DATE: 24-Jan-2000
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: EP 95 11 3021.0
    FILING DATE: 18-AUG-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Colin G. Sandercock, Esq.
    REGISTRATION NUMBER: 31,298
    REFERENCE/DOCKET NUMBER: 37629-0005
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (202) 912-2000
    TELEFAX: (202) 912-2020
  INFORMATION FOR SEQ ID NO: 26:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 119 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

Alignment Scores:
Pred. No.:   0.009   Length: 119
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 4   Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-070A-26 (1-119)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGCCGG------ 54
         ||||||||||||||||||||||||||||||| ||||||||||||||||:::
Db   50 IleIleTyrProGlyAspSerAspThrArgThrTyrSerProSerPheGlnGlyGlnValThr 69

Qy   55 ------GCGAGTCAGGTATTAGCAGC-----------TGG 78
         ||| :: ||||||:::
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 7
US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
  GENERAL INFORMATION:
    APPLICANT: Knappik, Achim
              Pack, Peter
              Ilag, Vic
              Ge, Liming
              Moroney, Simon
              Plueckthun, Andreas
  TITLE OF INVENTION: Protein/(Poly)peptide libraries
  NUMBER OF SEQUENCES: 373
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
    STREET: 1251 Avenue of the Americas
    CITY: New York
    STATE: New York
    COUNTRY: USA
    ZIP: 10021
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/490,153
    FILING DATE: 24-Jan-2000
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/025,769B
    FILING DATE: 18-FEB-1998
    APPLICATION NUMBER: EP 95 11 3021.0
    FILING DATE: 18-AUG-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: James F. Haley, Jr., Esq.
    REGISTRATION NUMBER: 27,794
    REFERENCE/DOCKET NUMBER: MORPHO/5
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212)596-9000
    TELEFAX: (212)596-9090
  INFORMATION FOR SEQ ID NO: 26:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 119 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

Alignment Scores:
Pred. No.:   0.009   Length: 119
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 4   Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-153-26 (1-119)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGCCGG------ 54
         ||||||||||||||||||||||||||||||| ||||||||||||||||:::
Db   50 IleIleTyrProGlyAspSerAspThrArgThrTyrSerProSerPheGlnGlyGlnValThr 69

Qy   55 ------GCGAGTCAGGTATTAGCAGC-----------TGG 78
         ||| ::: ||||||:::
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 8
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
  GENERAL INFORMATION:
    APPLICANT: Knappik, Achim
              Pack, Peter
              Ilag, Vic
              Ge, Liming

Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

Alignment Scores:
Pred. No.:   0.009   Length: 119
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 4   Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-324-26 (1-119)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
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Db 50 IleIleTyrProGlyAspSerAspThrArgThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy 55 ------GCGAGTCAGGGTATTAGCAGC------TGG 78
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Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 9
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-40

Alignment Scores:
Pred. No.:   0.00902   Length: 120
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 3   Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-025-769B-40 (1-120)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlyGlnValThr 69

Qy 55 ------GCGAGTCAGGGTATTAGCAGC------TGG 78
            ::: ||||||||||| |||
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 10
US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/09/025,769B
FILING DATE:  18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  EP 95 11 3021.0
FILING DATE:  18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME:  James F. Haley, Jr., Esq.
REGISTRATION NUMBER:  27,794
REFERENCE/DOCKET NUMBER:  MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE:  (212)596-9000
TELEFAX:  (212)596-9090
INFORMATION FOR SEQ ID NO:  67:
SEQUENCE CHARACTERISTICS:
LENGTH:  120 amino acids
TYPE:  amino acid
TOPOLOGY:  linear
MOLECULE TYPE:  protein
US-09-025-769B-67
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Alignment Scores:
Pred. No.:              0.00902      Length:          120
Score:                 92.20        Matches:         20
Percent Similarity:    67.65%       Conservative:    3
Best Local Similarity: 58.82%       Mismatches:      3
Query Match:           62.30%       Indels:          8
DB:                                 Gaps:            2
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NOLAN463-2A.SEQ (1-84) x US-09-025-769B-67 (1-120)

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Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
          ||||||||||||||||||||||     ||||||||||||||||||||||||||:::
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyValThr 69

Qy   55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
              ||  ::: ||||||||          |||
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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RESULT 11
US-09-490-070A-40
; Sequence 67, Application US/09490070A
; Patent No. 6696248
GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40

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Alignment Scores:
Pred. No.:              0.00902      Length:          120
Score:                 92.20        Matches:         20
Percent Similarity:    67.65%       Conservative:    54
Best Local Similarity: 58.82%       Mismatches:      3
Query Match:           62.30%       Indels:          8
DB:                                 Gaps:            2
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NOLAN463-2A.SEQ (1-84) x US-09-490-070A-40 (1-120)

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Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
          ||||||||||||||||||||||     ||||||||||||||||||||||||||:::
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyValThr 69

Qy   55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
              ||  ::: ||||||||          |||
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
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RESULT 12
US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 6696248
GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:

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                    STRANDEDNESS: <Unknown>
                    TOPOLOGY: linear
                    MOLECULE TYPE: protein
                    SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40

Alignment Scores:
Pred. No.:             0.00902         Length:          120
Score:                 92.20           Matches:         20
Percent Similarity:    67.65%          Conservative:    3
Best Local Similarity: 58.82%          Mismatches:      3
Query Match:           62.30%          Indels:          8
DB:                    4               Gaps:            2

NOLAN463-2A.SEQ (1-84) x US-09-490-153-40 (1-120)

Qy  1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ TGG 78
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Qy 55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 14
US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
    APPLICANT: Knappik, Achim
               Pack, Peter
               Ilag, Vic
               Ge, Liming
               Moroney, Simon
               Plueckthun, Andreas
    TITLE OF INVENTION: Protein/(Poly)peptide libraries
    NUMBER OF SEQUENCES: 373
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
      STREET: 1251 Avenue of the Americas
      CITY: New York
      STATE: New York
      COUNTRY: USA
      ZIP: 10021
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/490,153
      FILING DATE: 24-Jan-2000
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/025,769B
      FILING DATE: 18-FEB-1998
      APPLICATION NUMBER: EP 95 11 3021.0
      FILING DATE: 18-AUG-1995
    ATTORNEY/AGENT INFORMATION:
      NAME: James F. Haley, Jr., Esq.
      REGISTRATION NUMBER: 27,794
      REFERENCE/DOCKET NUMBER: MORPHO/5
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212)596-9000
      TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 67:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 120 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67
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                    TELEPHONE: (202) 912-2000
                    TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 67:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 120 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

Alignment Scores:
Pred. No.:             0.00902         Length:          120
Score:                 92.25           Matches:         20
Percent Similarity:    67.65%          Conservative:    3
Best Local Similarity: 58.82%          Mismatches:      3
Query Match:           62.30%          Indels:          8
DB:                    4               Gaps:            2

NOLAN463-2A.SEQ (1-84) x US-09-490-070A-67 (1-120)

Qy  1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
Db 50 IleIleTyrProGlySerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy 55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 13
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
    APPLICANT: Knappik, Achim
               Pack, Peter
               Ilag, Vic
               Ge, Liming
               Moroney, Simon
               Plueckthun, Andreas
    TITLE OF INVENTION: Protein/(Poly)peptide libraries
    NUMBER OF SEQUENCES: 373
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
      STREET: 1251 Avenue of the Americas
      CITY: New York
      STATE: New York
      COUNTRY: USA
      ZIP: 10021
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/490,153
      FILING DATE: 24-Jan-2000
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/025,769B
      FILING DATE: 18-FEB-1998
      APPLICATION NUMBER: EP 95 11 3021.0
      FILING DATE: 18-AUG-1995
    ATTORNEY/AGENT INFORMATION:
      NAME: James F. Haley, Jr., Esq.
      REGISTRATION NUMBER: 27,794
      REFERENCE/DOCKET NUMBER: MORPHO/5
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212)596-9000
      TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 40:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 120 amino acids
    TYPE: amino acid
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normal

#000000

#000000

butt

miter

10px sans-serif

start

alphabetic

inherit

source-over

good

good

path

OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 4, 2005, 19:01:38 ; Search time 78.75 Seconds
(without alignments)
832.849 Million cell updates/sec

Title: NOLAN463-2A.SEQ
Perfect score: 148
Sequence: 1 ATCATCTATCCTGGTGACTC.........GTATTAGCAGCTGGTTAGCC 84

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Searched: 1752860 seqs, 39097842 residues

Total number of hits satisfying chosen parameters: 3505720

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
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21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	97.9	66.1	116	10	US-09-851-614-4	Sequence 4, Appli
2	97.9	66.1	116	14	US-10-035-637-4	Sequence 4, Appli
3	97.9	66.1	116	16	US-10-769-144-4	Sequence 12, Appli
4	97.9	66.1	411	16	US-10-769-144-12	Sequence 12, Appl
5	97.9	66.1	468	16	US-10-769-144-2	Sequence 2, Appli
6	97.9	66.1	613	16	US-10-769-144-10	Sequence 10, Appl
7	96.2	65.0	118	17	US-10-726-332-29	Sequence 29, Appl
8	95.4	64.5	129	14	US-10-041-860-29	Sequence 29, Appl
9	95.4	64.5	129	14	US-10-041-860-215	Sequence 215, App
10	95.4	64.5	129	14	US-10-041-860-250	Sequence 250, App
11	95.4	64.5	129	14	US-10-041-860-319	Sequence 319, App
12	95.4	64.5	129	16	US-10-665-383-38	Sequence 38, Appl
13	94.9	64.1	116	17	US-10-727-155-100	Sequence 100, App
14	93.8	63.4	118	17	US-10-726-332-3	Sequence 3, Appli
15	93.5	63.2	118	17	US-10-726-332-5	Sequence 5, Appli
16	93.5	63.2	118	17	US-10-726-332-13	Sequence 13, Appl
17	93.5	63.2	118	17	US-10-726-332-139	Sequence 139, App
18	93.5	63.2	120	17	US-10-638-265-62	Sequence 62, Appl
19	93.5	63.2	120	17	US-10-638-265-78	Sequence 78, Appl
20	93.2	63.0	123	16	US-10-466-242-49	Sequence 49, Appl
21	93.2	63.0	301	14	US-10-002-631C-114	Sequence 114, App
22	92.4	62.4	225	16	US-10-128-520-158	Sequence 158, App
23	92.3	62.3	82	14	US-10-078-958-5	Sequence 5, Appli
24	92.2	62.3	98	14	US-10-194-975-45	Sequence 45, Appl
25	92.2	62.3	98	14	US-10-125-687-16	Sequence 16, Appl
26	92.2	62.3	98	14	US-10-041-860-6	Sequence 6, Appli
27	92.2	62.3	98	14	US-10-041-860-301	Sequence 301, App
28	92.2	62.3	98	14	US-10-041-860-302	Sequence 302, App
29	92.2	62.3	98	14	US-10-041-860-312	Sequence 312, App
30	92.2	62.3	98	14	US-10-041-860-314	Sequence 314, App
31	92.2	62.3	98	14	US-10-041-860-318	Sequence 318, App
32	92.2	62.3	98	14	US-10-041-860-320	Sequence 320, App
33	92.2	62.3	98	14	US-10-041-860-336	Sequence 336, App
34	92.2	62.3	98	14	US-10-041-860-338	Sequence 338, App
35	92.2	62.3	98	14	US-10-041-860-367	Sequence 367, App
36	92.2	62.3	98	15	US-10-308-817-88	Sequence 88, Appl
37	92.2	62.3	98	15	US-10-032-037B-106	Sequence 106, App
38	92.2	62.3	98	15	US-10-032-037B-108	Sequence 108, App
39	92.2	62.3	98	15	US-10-029-988B-106	Sequence 106, App
40	92.2	62.3	98	15	US-10-029-988B-108	Sequence 108, App
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42	92.2	62.3	98	15	US-10-032-423A-108	Sequence 108, App
43	92.2	62.3	98	15	US-10-453-698-88	Sequence 88, Appl
44	92.2	62.3	98	15	US-10-029-926B-106	Sequence 106, App
45	92.2	62.3	98	15	US-10-029-926B-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ.ID NO 4

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;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-851-614-4

Alignment Scores:
Pred. No.:                  0.0173        Length:           116
Score:                      97.90         Matches:          19
Percent Similarity:         36.84%        Conservative:     2
Best Local Similarity:      33.33%        Mismatches:       5
Query Match:                66.15%        Indels:           31
DB:                         10            Gaps:             1

NOLAN463-2A.SEQ (1-84) x US-09-851-614-4 (1-116)

Qy     1 ATCATCTATCCTGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC---------  51
         ||||||||||||||||||||||||  |||||||||||||
Db    50 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr  69

Qy    51 ---------------------------------------------------          51
Db    70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer  89

Qy    52 ------------CGGGCGAGTCAGGGTATTAGCAGCTGG  78
                     ::||||::||
Db    90 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106
```

```
Db    90 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106

RESULT 3
US-10-769-144-4
;  Sequence 4, Application US/10769144
;  Publication No. US20040248215A1
;  GENERAL INFORMATION:
;    APPLICANT: Keler, Tibor
;    APPLICANT: Endres, Michael
;    APPLICANT: He, Lizhen
;    APPLICANT: Ramakrishna, Venky
;    TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;    TITLE OF INVENTION: THEREFOR
;    FILE REFERENCE: MXI-301
;    CURRENT APPLICATION NUMBER: US/10/769,144
;    CURRENT FILING DATE: 2004-01-30
;    PRIOR APPLICATION NUMBER: 60/443979
;    PRIOR FILING DATE: 2003-01-31
;    NUMBER OF SEQ ID NOS: 32
;    SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 4
;    LENGTH: 116
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-769-144-4

Alignment Scores:
Pred. No.:                  0.0173        Length:           116
Score:                      97.90         Matches:          19
Percent Similarity:         36.84%        Conservative:     2
Best Local Similarity:      33.33%        Mismatches:       5
Query Match:                66.15%        Indels:           31
DB:                         16            Gaps:             1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-4 (1-116)

Qy     1 ATCATCTATCCTGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC---------  51
         ||||||||||||||||||||||||  |||||||||||||
Db    50 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr  69

Qy    51 ---------------------------------------------------          51
Db    70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer  89

Qy    52 ------------CGGGCGAGTCAGGGTATTAGCAGCTGG  78
                    :::||||||
Db    90 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106
```

```
RESULT 4
US-10-769-144-12
;  Sequence 12, Application US/10769144
;  Publication No. US20040248215A1
;  GENERAL INFORMATION:
;    APPLICANT: Keler, Tibor
;    APPLICANT: Endres, Michael
;    APPLICANT: He, Lizhen
;    APPLICANT: Ramakrishna, Venky
;    TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;    TITLE OF INVENTION: THEREFOR
;    FILE REFERENCE: MXI-301
;    CURRENT APPLICATION NUMBER: US/10/769,144
;    CURRENT FILING DATE: 2004-01-30
;    PRIOR APPLICATION NUMBER: 60/443979
;    PRIOR FILING DATE: 2003-01-31
;    NUMBER OF SEQ ID NOS: 32
;    SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 12
;    LENGTH: 411
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-769-144-12

Alignment Scores:
```

```
RESULT 2
US-10-035-637-4
;  Sequence 4, Application US/10035637
;  Publication No. US20030031667A1
;  GENERAL INFORMATION:
;    APPLICANT: Deo, Yashwant M.
;    APPLICANT: Keler, Tibor
;    TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
;    TITLE OF INVENTION: CELLS
;    FILE REFERENCE: MXI-166CP
;    CURRENT APPLICATION NUMBER: US/10/035,637
;    CURRENT FILING DATE: 2001-11-07
;    PRIOR APPLICATION NUMBER: 09/851,614
;    PRIOR FILING DATE: 2001-03-08
;    PRIOR APPLICATION NUMBER: USSN 60/203,126
;    PRIOR FILING DATE: 2000-05-08
;    PRIOR APPLICATION NUMBER: USSN 60/230,739
;    PRIOR FILING DATE: 2000-09-07
;    NUMBER OF SEQ ID NOS: 9
;    SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 4
;    LENGTH: 116
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-035-637-4

Alignment Scores:
Pred. No.:                  0.0173        Length:           116
Score:                      97.90         Matches:          19
Percent Similarity:         36.84%        Conservative:     2
Best Local Similarity:      33.33%        Mismatches:       5
Query Match:                66.15%        Indels:           31
DB:                         14            Gaps:             1

NOLAN463-2A.SEQ (1-84) x US-10-035-637-4 (1-116)

Qy     1 ATCATCTATCCTGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC---------  51
         ||||||||||||||||||||||||  |||||||||||||
Db    50 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr  69

Qy    51 ---------------------------------------------------          51
Db    70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer  89

Qy    52 ------------CGGGCGAGTCAGGGTATTAGCAGCTGG  78
                    :::||||::||
```

```
Pred. No.:              0.0236          Length:          411
Score:                  97.90           Matches:         19
Percent Similarity:     36.84%          Conservative:    2
Best Local Similarity:  33.33%          Mismatches:      5
Query Match:            66.15%          Indels:          31
DB:                     16              Gaps:            1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-12 (1-411)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC------ 51
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  191 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyValThr 210

Qy   51 ----------------------------- 51
Db  211 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 230

Qy   52 -------------CGGGCGAGTCAGGGTATTAGCAGCTGG 78
                     |||    :::||||:::      |||
Db  231 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 247
```

RESULT 5
US-10-769-144-2
; Sequence 2, Application US20040248215A1
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-2

```
Alignment Scores:
Pred. No.:              0.0244          Length:          468
Score:                  97.90           Matches:         19
Percent Similarity:     36.84%          Conservative:    2
Best Local Similarity:  33.33%          Mismatches:      5
Query Match:            66.15%          Indels:          31
DB:                     16              Gaps:            1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-2 (1-468)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC------ 51
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   69 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyValThr 88

Qy   51 ----------------------------- 51
Db   89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108

Qy   52 -------------CGGGCGAGTCAGGGTATTAGCAGCTGG 78
                     |||    :::||||:::      |||
Db  109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125
```

RESULT 6
US-10-769-144-10
; Sequence 10, Application US20040248215A1
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-10

```
Alignment Scores:
Pred. No.:              0.026           Length:          613
Score:                  97.90           Matches:         19
Percent Similarity:     36.84%          Conservative:    2
Best Local Similarity:  33.33%          Mismatches:      5
Query Match:            66.15%          Indels:          31
DB:                     16              Gaps:            1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-10 (1-613)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC------ 51
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   69 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyValThr 88

Qy   51 ----------------------------- 51
Db   89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108

Qy   52 -------------CGGGCGAGTCAGGGTATTAGCAGCTGG 78
                     |||    :::||||:::      |||
Db  109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125
```

RESULT 7
US-10-726-332-29
; Sequence 29, Application US/10726332
; Publication No. US2005008649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-29

Alignment Scores:
Pred. No.:   0.0275   Length: 118
Score: 96.20   Matches: 21
Percent Similarity: 67.65%   Conservative: 2
Best Local Similarity: 61.76%   Mismatches: 3
```

```
Query Match:                    65.00%     Indels:              8
DB:                             17         Gaps:                2

NOLAN463-2A.SEQ (1-84) x US-10-726-332-29 (1-118)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCGTCCTTCCAAGGCCCG------ 54
         |||||||||||||||||||||||||||||||||||||| |||||||||||:::
Db  50 IleIleTyrProGlySerAspThrArgTyrSerProSerPheGlnGlyGlnValThr   69

Qy  55 ------GCCAGTCAGGGTATTAGCAGC---------TGG 78
            ||| ||||||||||||       |||
Db  70 IleSerAlaAspGlnSerIleSerThrAlaTyrLeuGlnTrp 83
```

RESULT 8
US-10-041-860-29
; Sequence 29, Application US10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-29

```
Alignment Scores:
Pred. No.:                     0.0348      Length:            129
Score:                         95.40       Matches:            20
Percent Similarity:            57.50%      Conservative:        3
Best Local Similarity:         50.00%      Mismatches:          1
Query Match:                   64.46%      Indels:             16
DB:                            14          Gaps:                1

NOLAN463-2A.SEQ (1-84) x US-10-041-860-29 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCGTCCTTCCAAGGCCGGGCGGAGT 60
         |||||||||||||||||||||||||||||||||||||| |||||||||||:::
Db  50 IleIleTyrProGlySerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr    69

Qy  61 CAGGGTATTAGCAGC---------TGG 78
            |||||::::          |||
Db  70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
```

RESULT 9
US-10-041-860-215
; Sequence 215, Application US10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 215
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-215

```
Alignment Scores:
Pred. No.:                     0.0348      Length:            129
Score:                         95.40       Matches:            20
Percent Similarity:            57.50%      Conservative:        3
Best Local Similarity:         50.00%      Mismatches:          1
Query Match:                   64.46%      Indels:             16
DB:                            14          Gaps:                1

NOLAN463-2A.SEQ (1-84) x US-10-041-860-215 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGGAGT 60
         |||||||||||||||||||||||||||||||||||||| |||||||||||:::
Db  50 IleIleTyrProGlySerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr    69

Qy  61 CAGGGTATTAGCAGC---------TGG 78
            |||||::::          |||
Db  70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
```

RESULT 10
US-10-041-860-250
; Sequence 250, Application US2003015710A1
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 250
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-250

```
Alignment Scores:
Pred. No.:                     0.0348      Length:            129
Score:                         95.40       Matches:            20
Percent Similarity:            57.50%      Conservative:        3
Best Local Similarity:         50.00%      Mismatches:          1
Query Match:                   64.46%      Indels:             16
DB:                            14          Gaps:                1

NOLAN463-2A.SEQ (1-84) x US-10-041-860-250 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGGAGT 60
         |||||||||||||||||||||||||||||||||||||| |||||||||||:::
Db  50 IleIleTyrProGlySerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr    69

Qy  61 CAGGGTATTAGCAGC---------TGG 78
            |||||::::          |||
Db  70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
```

RESULT 11

US-10-041-860-319
; Sequence 319, Application US/10041860
; Publication No. US2003015710 9A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-319

Alignment Scores:
Pred. No.:   0.0348
Score: 95.40
Percent Similarity: 57.50%
Best Local Similarity: 50.00%
Query Match: 64.46%
DB: 14

NOLAN463-2A.SEQ (1-84) x US-10-041-860-319 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69

Qy   61 CAGGGTATTAGCAGC------------------------------------TGG 78
            ||||:::
Db   70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

                          Length: 129
                          Matches: 20
                          Conservative: 3
                          Mismatches: 1
                          Indels: 16
                          Gaps: 1

RESULT 12
US-10-665-383-38
; Sequence 38, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochelle, William
; APPLICANT: Lichtenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-38

Alignment Scores:
Pred. No.:   0.0348
Score: 95.40
Percent Similarity: 57.50%
Best Local Similarity: 50.00%

Query Match: 64.46%   Indels: 16
DB: Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-665-383-38 (1-129)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69

Qy   61 CAGGGTATTAGCAGC------------------------------------TGG 78
            ||||:::
Db   70 ------IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 13
US-10-727-155-100
; Sequence 100, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcook
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulencho
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-100

Alignment Scores:
Pred. No.:   0.0388   Length: 116
Score: 94.90   Matches: 19
Percent Similarity: 36.84%   Conservative: 2
Best Local Similarity: 33.33%   Mismatches: 5
Query Match: 64.12%   Indels: 31
DB: 17   Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-727-155-100 (1-116)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC----------- 51
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy   51 -- 51
Db   70 IleSerAlaAspLysSerIleThrThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89

Qy   52 ------CGGGGCGAGTCAGGGTATTAGCAGCTGG 78
            |||::: |||
Db   90 AspThrAlaMetTyrTyrCysAlaArgSerGlyTyrGlyMetAspValTrp 106

RESULT 14
US-10-726-332-3
; Sequence 3, Application US/10726332

```
; Publication No. US2005058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT: Mary Haak-Frendscho
;  APPLICANT: Ling Chen
;  APPLICANT: Yen-Wah R. Lee
;  APPLICANT: Meina Liang
;  APPLICANT: Xiao Feng
;  APPLICANT: Xiao-Chi Jia
;  APPLICANT: Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;  LENGTH: 118
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-726-332-3

Alignment Scores:
Pred. No.:                        0.0523          Length:           118
Score:                           93.80            Matches:          19
Percent Similarity:              36.21%           Conservative:     2
Best Local Similarity:           32.76%           Mismatches:       5
Query Match:                     63.38%           Indels:           32
DB:                              17               Gaps:             1

NOLAN463-2A.SEQ (1-84) x US-10-726-332-3 (1-118)

Qy       1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCGGGCG--- 57
           ||||||||||||||||||||||||||  ||||||||||||||||||||||||||:::
Db      50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy      57 --------------------------------------------------------- 57
Db      70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89

Qy      58 --------------------AGTCAGGGTATTAGCCAGCTGG 78
                               |||  |||:::   |||
Db      90 AspThrAlaMetTyrTyrCysAlaArgHisTrpSerTyrGlyMetAspValTrp 107

RESULT 15
US-10-726-332-5
; Sequence 5, Application US/10726332
; Publication No. US2005058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT: Mary Haak-Frendscho
;  APPLICANT: Ling Chen
;  APPLICANT: Yen-Wah R. Lee
;  APPLICANT: Meina Liang
;  APPLICANT: Xiao Feng
;  APPLICANT: Xiao-Chi Jia
;  APPLICANT: Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;  LENGTH: 118
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-726-332-5

Alignment Scores:
Pred. No.:                        0.0567          Length:           118
Score:                           93.50            Matches:          21
Percent Similarity:              45.10%           Conservative:     2
Best Local Similarity:           41.18%           Mismatches:       3
Query Match:                     63.18%           Indels:           25
DB:                              17               Gaps:             2

NOLAN463-2A.SEQ (1-84) x US-10-726-332-5 (1-118)

Qy       1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG----- 54
           ||||||||||||||||||||||||||  ||||||||||||||||||||||||:::
Db      50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy      55 ------GCGAGTCAGGGTATTAGC------------------------------------ 72
                 ||| ::: |||||
Db      70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89

Qy      73 -------AGCTGG 78
                  ||||||
Db      90 AspThrAlaMetTyrTyrCysAlaArgSerTrp 100

Search completed: August  4, 2005, 19:30:17
Job time : 80.75 secs
```

```
                    GenCore version 5.1.6
              Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August  4, 2005, 18:42:17 ; Search time 17.75 Seconds
                                         (without alignments)
                                      910.671 Million cell updates/sec

Title:         NOLAN463-2A.SEQ
Perfect score: 148
Sequence:      1 ATCATCTATCCTGGTGACTC........GTATTAGCAGCTGGTTAGCC 84

Scoring table: BLOSUM62
               Xgapop  10.0 , Xgapext   0.1
               Ygapop  10.0 , Ygapext   0.1
               Fgapop   6.0 , Fgapext   0.1
               Delop    6.0 , Delext    0.1

Searched:      283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:         566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123944_22592/app_query.fasta_1.5
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN 1_1.77 @runat_04082005_123944_22592 -NCPU=6  -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :     PIR_79:*
               1:  pir1:*
               2:  pir2:*
               3:  pir3:*
               4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Pred. No.	Score	Description
1	95.6	64.6	102	2	PH1281	15	92.2	62.3	102	2	PH1282	Ig heavy chain V r
2	95.6	64.6	102	2	PH1249	16	92.2	62.3	102	2	PH1248	Ig heavy chain V r
3	93.3	63.0	127	2	PH1409	17	92.2	62.3	102	2	PH1280	Ig heavy chain V r
4	93.2	63.0	127	2	PH1414	18	92.2	62.3	102	2	PH1258	Ig heavy chain V r
5	92.7	62.6	123	2	C36006	19	92.2	62.3	102	2	PH1264	Ig heavy chain V r
6	92.4	62.4	98	2	PH0877	20	92.2	62.3	102	2	PH1273	Ig heavy chain V r
7	92.3	62.3	98	2	PH1274	21	92.2	62.3	102	2	PH1271	Ig heavy chain V r
8	92.3	62.3	98	2	S26907	22	92.2	62.3	102	2	PH1278	Ig heavy chain V r
9	92.3	62.3	101	2	S12424	23	92.2	62.3	104	2	B36006	Ig heavy chain V r
10	92.2	62.3	102	2	PH1266	24	92.2	62.3	113	2	PH1428	Ig heavy chain V r
11	92.2	62.3	102	2	PH1279	25	92.2	62.3	115	2	PH1557	Ig heavy chain V pre
12	92.2	62.3	102	2	PH1277	26	92.2	62.3	117	2	A28846	Ig heavy chain pre
13	92.2	62.3	102	2	PH1244	27	92.2	62.3	117	2	S19670	Ig heavy chain - h
14	92.2	62.3	102	2	PH1272	28	92.2	62.3	123	2	PH1423	Ig heavy chain - h
						29	92.2	62.3	123	2	S38492	Ig heavy chain V r
						30	92.2	62.3	127	2	PH1411	Ig heavy chain V r
						31	92.2	62.3	128	2	S16685	Ig heavy chain V r
						32	92.2	62.3	136	2	A49047	Ig heavy chain V r
						33	92.2	62.3	136	2	PH1559	Ig heavy chain V r
						34	92.2	62.3	139	2	PH1558	Ig heavy chain V r
						35	91.4	61.8	101	2	S12428	Ig heavy chain V r
						36	90.4	61.1	102	2	PH1267	Ig heavy chain V r
						37	90.4	61.1	102	2	PH1259	Ig heavy chain V r
						38	90.4	61.1	134	2	PH1422	Ig heavy chain V r
						39	90.2	60.9	119	2	S36257	Ig heavy chain V r
						40	89.6	60.5	127	2	PH1420	Ig heavy chain V r
						41	89.2	60.3	102	2	PH1252	Ig heavy chain V r
						42	88.4	59.7	123	2	PH1413	Ig heavy chain V r
						43	88.2	59.6	102	2	PH1247	Ig heavy chain V r
						44	87.2	58.9	86	2	S12580	Ig heavy chain V r
						45	87.2	58.9	102	2	PH1265	Ig heavy chain V r

```
                              ALIGNMENTS

RESULT 1
PH1281
Ig heavy chain V region (clone PBL12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1281
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1281
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:                   0.00273          Length:          102
Score:                       95.60            Matches:         19
Percent Similarity:          77.78%           Conservative:    2
Best Local Similarity:       70.37%           Mismatches:      2
Query Match:                 64.59%           Indels:          4
DB:                          2                Gaps:            0

NOLAN463-2A.SEQ (1-84) x PH1281 (1-102)

Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGCGGCGAGT 60
         ||||||||||||||||||||||||| |||||||||||||||||  ||:::||
Db   54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGln---GlyGlnVa 72

Qy   61 CAGGGTATTAGCA 73
         :::|||||||||
Db   72 lThrIleLeuAla 76

RESULT 2
PH1249
```

Ig heavy chain V region (clone CORD7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1249
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1249
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
A;Note: the authors translated the stop codon for residue 5 as X
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00273   Length: 102
Score: 95.60   Matches: 19
Percent Similarity: 77.78%   Conservative: 2
Best Local Similarity: 70.37%   Mismatches: 2
Query Match: 64.59%   Indels: 4
DB: 2   Gaps: 0

NOLAN463-2A.SEQ (1-84) x PH1249 (1-102)

Qy   1 ATCATCTATCCTGGTGACTTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGCGAGT 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||| ::||
Db 54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGln----GlyGlnVa 72

Qy 61 CAGGGTATTAGCA 73
        |:||:||||||
Db 72 lThrIleLeuAla 76

RESULT 3
PH1409
Ig heavy chain V region (clone P1-51) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1409
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1409
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00533   Length: 127
Score: 93.30   Matches: 18
Percent Similarity: 70.00%   Conservative: 3
Best Local Similarity: 60.00%   Mismatches: 2
Query Match: 63.04%   Indels: 7
DB: 2   Gaps: 0

NOLAN463-2A.SEQ (1-84) x PH1409 (1-127)

Qy   1 ATCATCTATCCTGGTGACTTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGCGAGT 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyArgValThr 69

Qy 61 CAGGGTATTAGCAGCT 76
        ::::::|||
Db 70 ------MetSerAla 72

RESULT 4

PH1414
Ig heavy chain V region (clone P1-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1414
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1414
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
A;Experimental source: PBMC
A;Note: the authors translated the codon TTG for residue 119 as Met
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00548   Length: 127
Score: 93.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.97%   Indels: 8
DB: 2   Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1414 (1-127)

Qy   1 ATCATCTATCCTGGTGACTTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG---- 54
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyValThr 69

Qy 55 -----GCGAGTCAGGGTATTAGCAGC-----------TGG 78
        ||| |||||||||||
Db 70 IleSerAlaAspGluSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 5
C36006
Ig heavy chain V region (83p2) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: C36006
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36006
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <SCH>
A;Cross-references: GB:M34022
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00632   Length: 123
Score: 92.70   Matches: 19
Percent Similarity: 35.59%   Conservative: 2
Best Local Similarity: 32.20%   Mismatches: 5
Query Match: 62.64%   Indels: 33
DB: 2   Gaps: 1

NOLAN463-2A.SEQ (1-84) x C36006 (1-123)

Qy   1 ATCATCTATCCTGGTGACTTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
        ||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

```
Qy   54 ------------------------------------------------------------ 54

Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89

Qy   55 ------------------------GCCGAGTCAGGTATTAGCAGCTGG 78
                                 :::   |||  |||  |||
Db   90 AspThrAlaMetTyrTyrCysAlaAargHisAsnSerGlnThrGlyAlaSerLeuTrp 108
```

RESULT 6
PH0877
Ig heavy chain V region (anti-DNA, II-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 16-Aug-1996
C;Accession: PH0877
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0877
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <MAN>
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;50-66/Region: complementarity-determining 2

Alignment Scores:
Pred. No.:   0.00682   Length: 98
Score: 92.40   Matches: 18
Percent Similarity: 56.41%   Conservative: 4
Best Local Similarity: 46.15%   Mismatches: 1
Query Match: 62.43%   Indels: 16
DB: 2   Gaps: 1

NOLAN463-2A.SEQ (1-84) x PH0877 (1-98)

```
Qy    4 ATCATCTCGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGGCGGGGCGAGTCAG 63
        :::||||||||||||||||||||||||||||||||||||||||||||:::     :::
Db   51 ValTyrProGlyAspSerAspThrThrTyrTyrSerProSerPheGlnGlyGlnValThr--- 69

Qy   64 GGTATTAGCAGC----------TGG 78
         |||  |||  |||
Db   70 ---IleSerAlaAspLysCysIleSerThrAlaTyrLeuGlnTrp 83
```

RESULT 7
PH1274
Ig heavy chain V region (clone PBL5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 16-Aug-1996
C;Accession: PH1274
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1274
A;Molecule type: DNA
A;Residues: 1-98 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.:   0.00722   Length: 98
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 2   Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1274 (1-98)

```
Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGGCGG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73

Qy   55 -----GCCGAGTCAGGTATTAGCAGC----------TGG 78
             |||   |:::   ||||| |||   |||
Db   74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87
```

RESULT 8
S26907
Ig heavy chain V region (DP-73) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26907
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26907
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z13373; NID:g32965; PIDN:CAA78243.1; PID:g32966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00722   Length: 98
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 2   Gaps: 2

NOLAN463-2A.SEQ (1-84) x S26907 (1-98)

```
Qy    1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGGCGG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy   55 -----GCCGAGTCAGGTATTAGCAGC----------TGG 78
             |||   |:::   ||||| |||   |||
Db   70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
```

RESULT 9
S12424
Ig heavy chain V region (5) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C;Accession: S12424; S12425; S12426; S12427; S12429; S12432
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12424
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Cross-references: EMBL:X56372
A;Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT
A;Accession: S12425
A;Status: translation not shown
A;Accession: S12426
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA3>
A;Cross-references: EMBL:X56370
A;Accession: S12427

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA4>
A;Cross-references: EMBL:X56368
A;Accession: S12429
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA5>
A;Cross-references: EMBL:X56369
A;Accession: S12432
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA6>
A;Cross-references: EMBL:X56371
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00723   Length: 101
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 2   Gaps: 2

NOLAN463-2A.SEQ (1-84) x S12424 (1-101)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
          |||||||||||||||||||||||| ||||||||| |||||||||||||||:::
Db   53 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 72

Qy   55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
              ::: |||||||||||||||||::: |||
Db   73 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 86

RESULT 10
PH1266
Ig heavy chain V region (clone VERG5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1266
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1266
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00723   Length: 102
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 2   Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1266 (1-102)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
          ||||||||||||||||||||||||||||||||| |||||||||||||||:::
Db   54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73

Qy   55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
              ::: |||||||||||||||||::: |||
Db   74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87

RESULT 11

PH1279
Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1279
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: S12432
A;Accession: PH1279
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00723   Length: 102
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 2   Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1279 (1-102)

Qy   1 ATCATCTATCCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
          |||||||||||||||||||||||||| ||||||||||||||:::
Db   54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73

Qy   55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
              ::: |||||||||||||||||::: |||
Db   74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87

RESULT 12
PH1277
Ig heavy chain V region (clone PBL8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1277
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00723   Length: 102
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: 2   Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1277 (1-102)

Qy   1 ATCATCTATCCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
          |||||||||||||||||||||||||| ||||||||||||||:::
Db   54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73

Qy   55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
              ::: |||||||||||||||||::: |||
Db   74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87

RESULT 13
PH1244

Ig heavy chain V region (clone CORD2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1244
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro...
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1244
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00723   Length: 102
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1244 (1-102)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
         ||||||||||||||||||||||||||||||||||||||||||||||||:::
Db 54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73

Qy 55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
         ||| ::: ||||||:::|||
Db 74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87

RESULT 14
PH1272
Ig heavy chain V region (clone PBL3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1272
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro...
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1272
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00723   Length: 102
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1272 (1-102)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
         ||||||||||||||||||||||||||||||||||||||||||||||||:::
Db 54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73

Qy 55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
         ||| ::: ||||||:::|||
Db 74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87

RESULT 15
PH1282
Ig heavy chain V region (clone PBL13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro...
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00723   Length: 102
Score: 92.20   Matches: 20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82%   Mismatches: 3
Query Match: 62.30%   Indels: 8
DB: Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1282 (1-102)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGG------ 54
         ||||||||||||||||||||||||||||||||||||||||||||||||:::
Db 54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73

Qy 55 ------GCGAGTCAGGGTATTAGCAGC-----------TGG 78
         ||| ::: ||||||:::|||
Db 74 IleSerAlaAspLysSerIleSerThrThrTyrLeuGlnTrp 87

Search completed: August 4, 2005, 19:02:36
Job time : 18.75 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:23:15 ; Search time 80.75 Seconds
(without alignments)
1065.378 Million cell updates/sec

Title: NOLAN463-2A.SEQ
Perfect score: 148
Sequence: 1 ATCATCTATCCTGGTGACTC.........GTATTAGCAGCTGGTTAGCC 84

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123944_22581/app_query.fasta_1.5
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN 1_1_305 @runat_04082005_123944_22581 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :   UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70.3	47.5	118	2	Q9ZIC4	Q9zic4 mus musculu
2	68.3	46.1	111	2	Q9D9B8	Q9d9b8 mus musculu
3	68.3	46.1	474	2	Q8R3H6	Q8r3h6 mus musculu
4	67.6	45.7	236	2	Q6GMX8	Q6gmx8 homo sapien
5	67.3	45.5	614	2	Q7TMT6	Q7tmt6 mus musculu
6	64.4	42.4	302	2	Q9I9C3	Q9i9c3 anguilla an
c 7	63.6	43.0	117	1	KV1I_HUMAN	P01601 homo sapien
8	63.6	43.0	236	2	Q6PIH7	Q6pih7 mus musculu
9	63.5	42.9	473	2	Q7Q1B6	Q7q1b6 anopheles g
10	62.3	42.1	117	1	HV52_MOUSE	P06327 mus musculu
11	62.2	42.0	436	2	Q6TL49	Q6tl49 glyceria fl
c 12	62	41.9	138	2	Q72WG5	Q72wg5 desulfovibr
c 13	61.8	40.8	984	2	Q8MT62	Q8mt62 drosophila
14	61.8	40.7	1043	2	Q9VYS8	Q9vys8 drosophila
c 15	61.8	40.7	1059	2	Q76NS2	Q76ns2 drosophila
c 16	61.7	40.6	427	2	Q9AYR4	Q9ayr4 chaetoceros
c 17	61.7	40.6	427	2	Q9AYR6	Q9ayr6 chaetoceros
18	61.3	41.4	110	2	Q9JL83	Q9jl83 mus musculu
19	61	41.2	117	1	HV06_MOUSE	P01750 mus musculu
20	60.8	41.1	293	2	Q73WB2	Q73wb2 mycobacteri
21	60.6	40.9	324	2	Q7V9E2	Q7v9e2 prochloroco
c 22	60.5	39.8	517	2	Q9Y781	Q9y781 coprinus ci
23	60.3	39.7	660	1	YG39_PSESM	Q886e0 pseudomonas
c 24	60	39.5	609	2	Q9ARZ1	Q9arz1 oryza sativ
c 25	60	39.5	624	2	Q9FMN8	Q9fmn8 arabidopsis
c 26	60	39.5	929	2	Q7F8S7	Q7f8s7 oryza sativ
27	59.9	40.5	240	2	Q7PKV0	Q7pkv0 anopheles g
28	59.9	40.5	882	2	Q7PUM0	Q7pum0 anopheles g
29	59.9	40.5	930	2	Q7PY03	Q7py03 anopheles g
30	59.8	40.4	244	2	Q65ZC8	Q65zc8 homo sapien
c 31	59.8	39.3	270	1	VMT1_DHVI1	Q01479 dhori virus
c 32	59.7	39.3	189	2	Q6ZR89	Q6zr89 homo sapien
33	59.7	40.3	354	2	O27328	O27328 methanobact
34	59.6	40.3	323	2	Q8LDS8	Q8lds8 arabidopsis
35	59.6	40.3	323	2	Q949U9	Q949u9 arabidopsis
36	59.6	40.3	353	2	Q9LFW2	Q9lfw2 arabidopsis
37	59.3	40.1	481	2	Q91WT1	Q91wt1 mus musculu
38	59.3	40.1	724	2	Q41384	Q41384 spinacia ol
39	59	39.9	460	2	Q66IF9	Q66if9 xenopus tro
40	58.8	39.7	161	2	Q6JH66	Q6jh66 ambystoma t
41	58.7	39.7	596	2	Q74C03	Q74c03 geobacter s
42	58.7	39.7	777	2	Q6EP64	Q6ep64 oryza sativ
43	58.7	39.7	793	2	Q7QXY1	Q7qxy1 giardia lam
44	58.6	39.6	117	1	KV1J_HUMAN	P01602 homo sapien
45	58.4	39.5	477	2	Q89HM1	Q89hm1 bradyrhizob

ALIGNMENTS

RESULT 1
Q9ZIC4

ID	Q9ZIC4	PRELIMINARY;	PRT;	118 AA.

AC Q9ZIC4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Mol. Immunol. 34:441-452(1997).
DR EMBL; U78801; AAD00293.1; -.
DR HSSP; P01751; 1NQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Alignment Scores:
Pred. No.:   12.1   Length: 118
Score: 70.30   Matches: 13
Percent Similarity: 62.07%   Conservative: 5
Best Local Similarity: 44.83%   Mismatches: 4
Query Match: 47.50%   Indels: 7
DB: 2   Gaps: 0

```
NOLAN463-2A.SEQ (1-84) x Q921C4 (1-118)

Qy    4 ATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGCCGGGGCCGAGTCAG 63
        |||||||||||| ||||||||| :::  ||::::||||::||||:|:::
Db   51 IleTyrProGlyAspGlyAspThrSerTyrThrGlnLysPheArgGlyLysAlaThr--- 69

Qy   64 GGTATTAGCAGCT 76
        ||| |||
Db   70 ----LeuThrAla 72

RESULT 2
Q9D9B8
ID   Q9D9B8             PRELIMINARY;      PRT;    111 AA.
AC   Q9D9B8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE   library, clone:1700110111 product:immunoglobulin heavy chain 6 (heavy
DE   chain of IgM), full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RG   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya M., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito O., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK007163; BAB24877.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   111 AA;   11976 MW;   874DDF7BD98BD7B2 CRC64;

Alignment Scores:
Pred. No.:                 21.5        Length:              111
Score:                     68.30       Matches:             13
Percent Similarity:        58.62%      Conservative:        4
Best Local Similarity:     44.83%      Mismatches:          5
Query Match:               46.15%      Indels:              7
DB:                        2           Gaps:                0

NOLAN463-2A.SEQ (1-84) x Q9D9B8 (1-111)

Qy    4 ATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGCCGGGGCCGAGTCAG 63
        |||||||||||| ||||||| :::  ||::: ||||::||||:|:::
Db   57 IleTyrProGlyAspThrAsnTyrAsnGlyLysPheLysGlyLysAlaThr--- 75

Qy   64 GGTATTAGCAGCT 76
        ||| |||
Db   76 ----LeuThrAla 78

RESULT 3
Q8R3H6
ID   Q8R3H6             PRELIMINARY;      PRT;    474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AU044919 protein.
GN   Name=AU044919;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
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RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
DR   HSSP; P01869; 1CL7.
DR   MGD; MGI:2144967; AU044919.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   474 AA;  51748 MW;  86D8B57C6CD2874A CRC64;

Alignment Scores:
Pred. No.:                 27.1          Length:        474
Score:                     68.30         Matches:       14
Percent Similarity:        55.17%        Conservative:  2
Best Local Similarity:     48.28%        Mismatches:    6
Query Match:               46.15%        Indels:        7
DB:                        2             Gaps:          0

NOLAN463-2A.SEQ (1-84) x Q8R3H6 (1-474)

Qy   4 ATCTATCCTGGTGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGCCGGCGGAGTCAG 63
         ||::||||||||| |||||| ||||| |||||:||||| ||||||| ||||||:|||
Db  70 IlePheProGlyAspGlyAspThrHisTyrSerGlyLysPheGlnGlyLysAlaLys--- 88

Qy  64 GGTATTAGCAGCT 76
         ||| |||
Db  89 ---LeuThrAla 91

RESULT 4
Q6GMX8
ID   Q6GMX8         PRELIMINARY;     PRT;    236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
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RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

Alignment Scores:
Pred. No.:                 29.7          Length:        236
Score:                     67.60         Matches:       18
Percent Similarity:        47.50%        Conservative:  1
Best Local Similarity:     45.00%        Mismatches:    7
Query Match:               45.68%        Indels:        14
DB:                        2             Gaps:          2

NOLAN463-2A.SEQ (1-84) x Q6GMX8 (1-236)

Qy   7 TATCCTGGT--------GACTCTGATACCACCATACAGCCCGTCC---------- 42
         ||::||||||        ||       ||:|||||||||||||| ||||||||
Db  17 PheProGlySerArgCysAspIleGlnMetThrGlnSerProSerSerValSerAlaSer 36

Qy  43 ----------TTCCAAGGCCGGCGAGTCAGGTATTAGCAGCTGGTTAGCC 84
                   ||||||||||||||||||||||||||||||||||||||||||
Db  37 ValGlyAspArgValThrIleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAla 56

RESULT 5
Q7TMT6
ID   Q7TMT6         PRELIMINARY;     PRT;    614 AA.
AC   Q7TMT6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MGC60843 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
```

```
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA  Strausberg R.;
RL  Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC053409; AAH53409.1; -.
DR  HSSP; P01820; 1G7J.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF07654; C1-set; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS50835; IG_LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ  SEQUENCE   614 AA;  67746 MW;  839BAF3B8D124F89 CRC64;

Alignment Scores:
Pred. No.:                       37.8          Length:              614
Score:                           67.30         Matches:             12
Percent Similarity:              58.62%        Conservative:        5
Best Local Similarity:           41.38%        Mismatches:          5
Query Match:                     45.47%        Indels:              7
DB:                                            Gaps:                0

NOLAN463-2A.SEQ (1-84) x Q7TMT6 (1-614)

Qy     4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG 63
         ::||||||||||||| |||||  |||::||  ||||::||||::||||
Db    70 ValTyrProGlyAspGlyAspThrAsnTyrAsnGlyLysPheLysGlyLysAlaThr--- 88

Qy    64 GGTATTAGCAGCT 76
         ||| ||||
Db    89 ---LeuThrAla 91

RESULT 6
Q9I9C3
ID  Q9I9C3        PRELIMINARY;        PRT;   302 AA.
AC  Q9I9C3;
DT  01-OCT-2000 (TrEMBLrel. 15, Created)
DT  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Sodium/potassium-transporting ATPase beta-233 chain (Sodium/potassium-
DE  dependent ATPase beta-233 subunit).
GN  Name=atnb233;
OS  Anguilla anguilla (European freshwater eel).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC  Anguilla.
OX  NCBI_TaxID=7936;
RN  [1]
RP  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC  TISSUE=Gill;
RX  PubMed=10896885;
RA  Cutler C.P., Brezillon S., Bekir S., Sanders I.L., Hazon N., Cramb G.;
RT  "Expression of a duplicate Na,K-ATPase beta(1)-isoform in the European
RT  eel (Anguilla anguilla).";
RL  Am. J. Physiol. 279:R222-R229(2000).
CC  -!- FUNCTION: This is the non-catalytic component of the active
CC      enzyme, which catalyzes the hydrolysis of ATP coupled with the
CC      exchange of Na(+) and K(+) ions across the plasma membrane.
CC  -!- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
CC      gamma.
CC  -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC  -!- TISSUE SPECIFICITY: Expressed mainly in epithelial tissues.
CC  -!- SIMILARITY: Belongs to the Na+/K+ and H+/K+ ATPases beta chain
CC      family.
DR  EMBL; AJ239317; CAB85586.1; -.
DR  GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; NAS.
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DR  GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; NAS.
DR  GO; GO:0006813; P:potassium ion transport; NAS.
DR  GO; GO:0006814; P:sodium ion transport; NAS.
DR  InterPro; IPR000402; Na/K_ATPase_beta.
DR  Pfam; PF00287; Na_K-ATPase; 1.
DR  TIGRFAMs; TIGR01107; Na_K-ATPase_bet; 1.
DR  PROSITE; PS00390; ATPASE_NA_K_BETA_1; 1.
DR  PROSITE; PS00391; ATPASE_NA_K_BETA_2; 1.
KW  Glycoprotein; Signal-anchor;  Sodium/potassium transport;
KW  Transmembrane.
FT  DOMAIN        1     33       CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM     34     54       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                              (POTENTIAL).
FT  DOMAIN       55    302       EXTRACELLULAR (POTENTIAL).
FT  DISULFID    125    148       By similarity.
FT  DISULFID    158    174       By similarity.
FT  DISULFID    213    274       By similarity.
FT  CARBOHYD    193    193       N-LINKED (GLCNAC...) (POTENTIAL).
FT  CARBOHYD    263    263       N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE   302 AA;  34706 MW;  721E056F04274D0D CRC64;

Alignment Scores:
Pred. No.:                       79.1          Length:              302
Score:                           64.40         Matches:             14
Percent Similarity:              26.15%        Conservative:        3
Best Local Similarity:           21.54%        Mismatches:          2
Query Match:                     42.37%        Indels:              46
DB:                                            Gaps:                2

NOLAN463-2A.SEQ (1-84) x Q9I9C3 (1-302)

Qy    61 GACTCGCCCGGC---------------------------CTTGGA 44
                                                 : ::
Db     6 AspSerAspGlyTrpLysThrPheIleTrpAsnSerGluLysGluLeuLysGly 25

Qy    43 AGGACGGCTGTATGTGGTATCAG-- 20
         ||||||||  ||||:||
Db    26 ArgThrGlyCysSerTrpPheLysIleLeuLeuLeuPheTyrValIlePheTyrGlyCysLeu 45

Qy    20 -------------------- 20

Db    46 AlaAlaValPheValGlyThrIleGlnAlaAlaLeuLeuThrLeuSerAsnTyrLysPro 65

Qy    19 AGTCACCAGGATAGA 5
         ::||||||||||||
Db    66 ThrHisGlnAspArg 70

RESULT 7
KV1I_HUMAN
ID  KV1I_HUMAN      STANDARD;       PRT;   117 AA.
AC  P01601;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-I region HK101 precursor (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81098966; PubMed=6779204;
RA  Bentley D.L., Rabbitts T.H.;
RT  "Human immunoglobulin variable region genes -- DNA sequences of two V
RT  kappa genes and a pseudogene.";
RL  Nature 288:730-733(1980).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
RA  Bentley D.L., Rabbitts T.H.;
RT  "Evolution of immunoglobulin V genes: evidence indicating that
RT  recently duplicated human V kappa sequences have diverged by gene
RT  conversion.";
```

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RL   Cell 32:181-189(1983).
CC
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; K01322; AAA58930.1; -.
DR   EMBL; K01324; AAA58932.1; -.
DR   EMBL; V00558; CAA23824.1; -.
DR   PIR; A01881; KIHU11.
DR   HSSP; P01607; 1BWW.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL         1     22
FT   CHAIN         23   >117       Ig kappa chain V-I region HK101.
FT   DOMAIN        23    45        Framework-1.
FT   DOMAIN        46    56        Complementarity-determining-1.
FT   DOMAIN        57    71        Framework-2.
FT   DOMAIN        72    78        Complementarity-determining-2.
FT   DOMAIN        79   110        Framework-3.
FT   DOMAIN       111   >117       Complementarity-determining-3.
FT   DISULFID      45   110        By similarity.
FT   NON_TER      117   117
SQ   SEQUENCE     117 AA;  12799 MW;  D7D0FF3718CEF587 CRC64;

Alignment Scores:
Pred. No.:              86                 Length:         117
Score:                  63.60              Matches:         17
Percent Similarity:     45.24%             Conservative:     2
Best Local Similarity:  40.48%             Mismatches:       9
Query Match:            42.97%             Indels:          14
DB:                     1                  Gaps:             2

NOLAN463-2A.SEQ (1-84) x KV1I_HUMAN (1-117)

Qy    1 ATCATCTATCCTGGT-----------GACTCTGATACCACCATACAGCCCGTCC----------- 42
          ::: :::||||||              ||      |||||||||||||  ||||||
Db   15 LeuCysPheProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSer 34

Qy   43 ------------TTCCAAGGCCGGGCAGTCAGGGTATTAGCAGCTGG 78
                     |||||||||||||||||
Db   35 AlaSerValGlyAspArgValThrIleThrCysArgAlaArgGlnGlnIleSerSerTrp 54

Qy   79 TTAGCC 84
          ||||||
Db   55 LeuAla 56

RESULT 8
Q6PIH7
ID   Q6PIH7     PRELIMINARY;     PRT;   236 AA.
AC   Q6PIH7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;

RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034141; AAH34141.1; -.
     HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE  236 AA;  25603 MW;  8BC56110686121 3F CRC64;

Alignment Scores:
Pred. No.:              96.2               Length:         236
Score:                  63.60              Matches:         18
Percent Similarity:     48.72%             Conservative:     1
Best Local Similarity:  46.15%             Mismatches:       6
Query Match:            42.97%             Indels:          14
DB:                     2                  Gaps:             2

NOLAN463-2A.SEQ (1-84) x Q6PIH7 (1-236)

Qy   10 CCTGGT-----------GACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC----------- 51
          ||||||              ||||||||||||||||||
Db   18 ProGlyAlaArgCysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerVal 37

Qy   52 -----------CGGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCC 84
                    ||||||||||||||  :::||||||
Db   38 GlyAspArgValThrIleThrCysArgAlaSerGlnGlyIleSerSerTyrLeuAla 56

RESULT 9
Q7Q1B6
ID   Q7Q1B6     PRELIMINARY;     PRT;   473 AA.
AC   Q7Q1B6;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP8180 (Fragment).
GN   Name=agCG51167; ORFNames=ENSANGG00000012318;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008980; EAA14419.1; -.
DR   InterPro; IPR005654; AFG1 ATPase.
DR   Pfam; PF03969; AFG1_ATPase; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   473 AA;  53210 MW;  6F8197395A1C7F79 CRC64;

Alignment Scores:
Pred. No.:                             Length:           473
Score:              111                Matches:           13
Percent Similarity: 63.50              Conservative:       4
Best Local Similarity: 44.74%          Mismatches:         6
Query Match:        34.21%             Indels:            15
                    42.91%             Gaps:               0
DB:                       2

NOLAN463-2A.SEQ (1-84) x Q7Q1B6 (1-473)

Qy   1 ATCATCTATCCTGGTGACTCTGATACCACAGCCCGTCCTTCCAAGGCCGGGCGAGT 60
         :::::|||      |||||| ||||||||||||||||||::: :|||
Db  84 ValValTyr------AspSerIleLysThrTyrSerPro------ProLysPro----Ser 98

Qy  61 CAGGGTATTAGCAGCTGGTTAGCC 84
         |||   ::|     ::: |||
Db  99 ThrGlyIleLysTrpPheSer 106

RESULT 10
HV52_MOUSE
ID   HV52_MOUSE     STANDARD;      PRT;   117 AA.
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region VH558 A1/A4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------
DR   EMBL; M13787; AAA38499.1; -.
DR   PIR; A02029; HVMSA1.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V region VH558 A1/A4.
FT   DOMAIN       20     49       Framework-1.
FT   DOMAIN       50     54       Complementarity-determining-1.
FT   DOMAIN       55     68       Framework-2.
FT   DOMAIN       69     85       Complementarity-determining-2.
FT   DOMAIN       86    117       Framework-3.
FT   DISULFID     41    115       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12971 MW;  8B0BC138856DFC9D CRC64;

Alignment Scores:
Pred. No.:                             Length:           117
Score:              126                Matches:           12
Percent Similarity: 62.30              Conservative:       4
Best Local Similarity: 55.17%          Mismatches:         6
Query Match:        41.38%             Indels:             7
                    42.09%             Gaps:               0
DB:                       1

NOLAN463-2A.SEQ (1-84) x HV52_MOUSE (1-117)

Qy   4 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAG 63
         ||||||||||||| |||||||||| |||||| |:::   |||:::||||:::||||:||
Db  70 IleTyrProGlyAspGlySerThrLysTyrAsnGluLysPheLysGlyLysAlaThr--- 88

Qy  64 GGTATTAGCAGCT 76
         |||   |||
Db  89 ---LeuThrAla 91

RESULT 11
Q6TL49
ID   Q6TL49         PRELIMINARY;      PRT;   436 AA.
AC   Q6TL49;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE   (Fragment).
GN   Name=rbcL;
OS   Glyceria fluitans.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Meliceae; Glyceria.
OX   NCBI_TaxID=254778;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dolphin K.P., Joseph J.A., Fay M.F., Purvis A., Gowing D.,
RA   Crawley M.J., Cowan R.S.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
CC       ribulose 1,5-bisphosphate, the primary event in photosynthetic
CC       carbon dioxide fixation, as well as the oxidative fragmentation of
CC       the pentose substrate in the photorespiration process. Both
CC       reactions occur simultaneously and in competition at the same
CC       active site (By similarity).
CC   -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
CC       2 3-phospho-D-glycerate.
CC   -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
CC       phospho-D-glycerate + 2-phosphoglycolate.
CC   -!- SUBUNIT: 8 large chains + 8 small chains (By similarity).
CC   -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC   -!- SIMILARITY: Belongs to the RuBisCO large chain family.
DR   EMBL; AY395539; AAR98681.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0009573; C:ribulose bisphosphate carboxylase complex (. . .; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   GO; GO:0004497; F:monooxygenase activity; IEA.
DR   GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
DR   GO; GO:0015977; P:carbon utilization by fixation of carbon di.. .; IEA.
DR   GO; GO:0009853; P:photorespiration; IEA.
DR   GO; GO:0015979; P:photosynthesis; IEA.
DR   InterPro; IPR000685; RuBisCO_large.
DR   Pfam; PF00016; RuBisCO_large; 1.
DR   Pfam; PF02788; RuBisCO_large_N; 1.
DR   PROSITE; PS00157; RUBISCO_LARGE; 1.
KW   Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
```

KW   Oxidoreductase; Photorespiration; Photosynthesis.
FT   NON_TER   1   1
FT   NON_TER   436   436
SQ   SEQUENCE   436 AA; 48417 MW; 229C3E9FFCB4420B CRC64;

Alignment Scores:
Pred. No.:   Length: 436
Score: 160   Matches: 13
Percent Similarity: 62.20%   Conservative: 2
Best Local Similarity: 39.47%   Mismatches: 5
Query Match: 34.21%   Indels: 18
DB: 42.03%   Gaps: 0
                       2

NOLAN463-2A.SEQ (1-84) x Q6TL49 (1-436)

Qy   7 TATCCTGGTGACTCTGATACCATACAGCCCGTCCTTCCAAGGCCGGGCGAGTCAGGGT 66
            ||| |||||||| |||||||:::||||||----------
Db   61 TyrLysGlyArgCys--TyrHisIleGluProVal---------ProGlyGluGluGly- 76

Qy   67 ATTAGCAGCTGGTTAGCC 84
           ||||||||:||:|||
Db   77 ------GlnTrpIleAla 80

RESULT 12
Q72WG5
ID   Q72WG5   PRELIMINARY;   PRT;   138 AA.
AC   Q72WG5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Sigma factor serine-protein kinase.
GN   OrderedLocusNames=DVUA0124;
OS   Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS   8303).
OG   Plasmid pDV.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC   Desulfovibrionaceae; Desulfovibrio.
OX   NCBI_TaxID=882;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15077118; DOI=10.1038/nbt959;
RA   Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA   Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA   Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA   Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA   Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
RA   Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA   Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT   "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT   Desulfovibrio vulgaris Hildenborough.";
RL   Nat. Biotechnol. 22:554-559(2004).
DR   EMBL; AE017286; AAS94340.1; -.
DR   TIGR; DVUA0124; -.
KW   Complete proteome.
SQ   SEQUENCE   138 AA; 15178 MW; 0878CD5858774397 CRC64;

Alignment Scores:
Pred. No.:   Length: 138
Score: 141   Matches: 12
Percent Similarity: 62.00%   Conservative: 0
Best Local Similarity: 41.38%   Mismatches: 7
Query Match: 41.38%   Indels: 10
DB: 40.79%   Gaps: 0
                       2

NOLAN463-2A.SEQ (1-138)

Qy   67 TACCCTGACTCGCCCGCCCTTGGAAGGACGGGCTGTATCGGTATCAGAGTCACCAGGAT   8
           |||||||||||||||| ||| ||||||
Db   51 TyrProAspSerProGlyLysAlaGluValGlyCys--------ArgValValLeuPh 67

Qy   7 AGATGAT 1
           ||||||
Db   67 eAspAsp 69

RESULT 13
Q8MT62
ID   Q8MT62   PRELIMINARY;   PRT;   984 AA.
AC   Q8MT62;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   RE04357p.
GN   ORFNames=CG10353;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY118358; AAM48387.1; -.
DR   FlyBase; FBgn0030349; CG10353.
DR   InterPro; IPR007632; DUF590.
DR   Pfam; PF04547; DUF590; 1.
SQ   SEQUENCE   984 AA; 112356 MW; 233EFCAAAD0405E8 CRC64;

Alignment Scores:
Pred. No.:   Length: 984
Score: 205   Matches: 13
Percent Similarity: 61.80%   Conservative: 6
Best Local Similarity: 55.88%   Mismatches: 3
Query Match: 38.24%   Indels: 12
DB: 40.66%   Gaps: 1
                       2

NOLAN463-2A.SEQ (1-84) x Q8MT62 (1-984)

Qy   77 CAGTCGCTAATACCCTGACTCGCCCGGCCTTGGAAGGAC-------------GGGCTG 33
           :::::::||||||| ||| ||| |||||::   :||||||
Db 685 GluMetLeuIleProTyrLeuMetArgThrPheLysGluLeuSerTyrArgHisGly--- 703

Qy   32 TATGTGGTATCAGAGTCACCAGGATAGA   5
           ||||:::|||||||||||||
Db 704 ---TrpTyrLysSerHisGlnAspGln 711

RESULT 14
Q9VYS8
ID   Q9VYS8   PRELIMINARY;   PRT;   1043 AA.
AC   Q9VYS8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CG10353-PA.
GN   ORFNames=CG10353;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

DR   EMBL; AE003487; AAF48110.2; -.
DR   IntAct; Q9VYS8; -.
DR   FlyBase; FBgn0030349; CG10353.
DR   InterPro; IPR007632; DUF590.
DR   Pfam; PF04547; DUF590; 1.
SQ   SEQUENCE   1043 AA; 118845 MW; 0EA6BDC5C219FF35 CRC64;

Alignment Scores:
Pred. No.:   207   Length: 1043
Score: 61.80   Matches: 13
Percent Similarity: 55.88%   Conservative: 6
Best Local Similarity: 40.66%   Mismatches: 3
Query Match: Indels: 12
DB: 2   Gaps: 1

NOLAN463-2A.SEQ (1-84) x Q9VYS8 (1-1043)

Qy   77 CAGCTGCTAATACCCTGACTCGCCCGGCCTTGGAAGGAC-----------GGGCTG 33
         ::::::||||||||| || ||| ||||||||:||||| |||
Db   744 GluMetLeuIleProTyrLeuMetArgThrPheLysGluLeuSerTyrArgHisGly--- 762

Qy   32 TATGTGGTATCAGAGTCACCAGGATAGA 5
         |||||||||||||:|||||||||:|::
Db   763 ---TrpTyrLysSerHisGlnAspGln 770

RESULT 15
ID   Q76NS2   PRELIMINARY;   PRT;   1059 AA.
AC   Q76NS2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CG10353-PB.
GN   ORFNames=CG10353;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
.   RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

Search completed: August 4, 2005, 19:01:24
Job time : 87.75 secs

RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003487; AAN09305.2; -.
DR   InterPro; IPR007632; DUF590.
DR   Pfam; PF04547; DUF590; 1.
SQ   SEQUENCE 1059 AA; 120767 MW; 67636566C1CA98A CRC64;

Alignment Scores:
Pred. No.:
Score: 207   Length: 1059
Percent Similarity: 61.80%   Matches: 13
Best Local Similarity: 55.88%   Conservative: 6
Query Match: 38.24%   Mismatches: 3
DB: 40.66%   Indels: 12
                   2   Gaps: 1

NOLAN463-2A.SEQ (1-84) x Q76NS2 (1-1059)

```
Qy    77 CAGCTGCTAATACCCTGACTCGCCCGGCCTTGGAAGGAC------------GGGCTG  33
         ::::|||||||  |||||| ||| |||| |||||||||   ::||||:||   ||||
Db   760 GluMetLeuIleProTyrLeuMetArgThrPheLysGluSerTyrArgHisGly--- 778

Qy    32 TATCTGGTATCAGAGTCACCAGGATAGA  5
         |||||||:::||||||||||||||::::
Db   779 ---TrpTyrLysSerHisGlnAspGln 786
```

```
          GenCore version 5.1.6
     Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:   August 4, 2005, 18:21:34 ; Search time 90 Seconds
                                       (without alignments)
                                       721.953 Million cell updates/sec

Title:          NOLAN463-2B.SEQ
Perfect score:  148
Sequence:     1 CGGGCGAGTCAGGGTATTAG.......ACAGCCCGTCCTTCCAAGGC 84

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.1
                Ygapop 10.0 , Ygapext  0.1
                Fgapop  6.0 , Fgapext  0.1
                Delop   6.0 , Delext   0.1

Searched:     2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:     4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123943_22574/app_query.fasta_1.5
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN 1_1 308 @runat 04082005 123943 22574 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Database : A_Geneseq_16Dec04:*
      1: geneseqp1980s:*
      2: geneseqp1990s:*
      3: geneseqp2000s:*
      4: geneseqp2001s:*
      5: geneseqp2002s:*
      6: geneseqp2002as:*
      7: geneseqp2003bs:*
      8: geneseqp2004s:*
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	115	77.7	123	5	ABG76561	Abg76561 HCV E1 an
2	113.3	76.6	411	8	ADR46829	Adr46829 Human pB1
3	106.2	71.8	122	4	AAU02582	Aau02582 Anti-adip
4	104.4	70.5	474	4	AAU14177	Aau14177 Human nov
5	103.4	69.9	98	2	AAW54008	Aaw54008 Human Ant
6	103.4	69.9	98	5	ABG78233	Abg78233 Human Fv
7	103.4	69.9	98	5	ABG78231	Abg78231 Human Fv
8	103.4	69.9	98	5	ABG78232	Abg78232 Human Fv
9	103.4	69.9	98	5	ABG91924	Abg91924 Human ant
10	103.4	69.9	98	5	ABG91922	Abg91922 Human ant
11	103.4	69.9	98	5	ABG91923	Abg91923 Human ant
12	103.4	69.9	98	5	ABU56809	Abu56809 Human Imm
13	103.4	69.9	98	6	ABP56508	Abp56508 Human ant
14	103.4	69.9	98	6	ABJ18687	Abj18687 Antibody
15	103.4	69.9	98	6	ABO27112	Abo27112 Human ger
16	103.4	69.9	98	7	ADD69247	Add69247 Human hea
17	103.4	69.9	98	7	ADF10156	Adf10156 Antibody
18	103.4	69.9	98	7	ADF09948	Adf09948 Antibody
19	103.4	69.9	98	7	ADF10053	Adf10053 VEGF anti
20	103.4	69.9	98	7	ADK18943	Adk18943 Anti-huma
21	103.4	69.9	98	7	ADK18888	Adk18888 Anti-huma
22	103.4	69.9	98	7	ADK18877	Adk18877 Anti-huma
23	103.4	69.9	98	7	ADK18878	Adk18878 Anti-huma
24	103.4	69.9	98	7	ADK18912	Adk18912 Anti-huma
25	103.4	69.9	98	7	ADK18582	Adk18582 Anti-huma
26	103.4	69.9	98	7	ADK18896	Adk18896 Anti-huma
27	103.4	69.9	98	7	ADK18894	Adk18894 Anti-huma
28	103.4	69.9	98	7	ADJ80328	Adj80328 VH gene 1
29	103.4	69.9	98	8	ADR46847	Adr46847 Human VH5
30	103.4	69.9	109	8	ADI05782	Adi05782 Human mon
31	103.4	69.9	109	8	ADP22377	Adp22377 Human ant
32	103.4	69.9	109	8	ADP22385	Adp22385 Human ant
33	103.4	69.9	109	8	ADS12513	Ads12513 Human Vh5
34	103.4	69.9	109	8	ADS12515	Ads12515 Human Vh5
35	103.4	69.9	109	8	ADS12514	Ads12514 Human Vh5
36	103.4	69.9	110	8	ADP47302	Adp47302 Human pho
37	103.4	69.9	113	6	ABU08149	Abu08149 Human Erb
38	103.4	69.9	113	7	ADD69211	Add69211 Human ant
39	103.4	69.9	116	8	ADP22194	Adp22194 Human ant
40	103.4	69.9	117	2	AAR66339	Aar66339 Human imm
41	103.4	69.9	117	4	AAG62966	Aag62966 Amino aci
42	103.4	69.9	117	5	AAO15186	Aao15186 Digi anti
43	103.4	69.9	117	8	ABP97450	Abp97450 Human ant
44	103.4	69.9	117	8	ADL70771	Adl70771 Anti-TNFa
45	103.4	69.9	117	8	ADP47229	Adp47229 Human pho

ALIGNMENTS

```
RESULT 1
ABG76561
ID   ABG76561 standard; protein; 123 AA.
XX
AC   ABG76561;
XX
DT   05-NOV-2002  (first entry)
XX
DE   HCV E1 antigen monoclonal antibody #49.
XX
KW   Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
KW   hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
XX
OS   Homo sapiens.
XX
PN   WO200260954-A1.
XX
PD   08-AUG-2002.
XX
PF   14-JAN-2002; 2002WO-SB000044.
XX
PR   12-JAN-2001; 2001US-0260889P.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Drakenberg K,  Persson MAA;
XX
DR   WPI; 2002-608502/65.
XX
PT   Vaccine comprising a human monoclonal antibody against hepatitis C virus
PT   (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
XX
PS   Disclosure; Page 54; 64pp; English.
XX
```

CC   The invention relates to a human monoclonal antibody or its antigen
CC   binding fragments, which exhibit immunological binding affinity for a
CC   hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
CC   homologous to the binding portion of a human antibody Fab molecule from a
CC   combinatorial antibody library. The vaccine composition comprising the
CC   antibodies or antigen binding fragments against HCV E1 or E2 antigen or
CC   its hypervariable region is useful in treating or preventing HCV
CC   infection in a subject. Sequences ABG76513-ABG76568 represent human
CC   monoclonal antibodies against HCV E1 antigen
XX
SQ   Sequence 123 AA;

Alignment Scores:
Pred. No.:   7.05e-05   Length: 123
Score: 115.00   Matches: 23
Percent Similarity: 55.32%   Conservative: 3
Best Local Similarity: 48.94%   Mismatches: 1
Query Match: 77.70%   Indels: 20
DB: Gaps: 1

NOLAN463-2B.SEQ (1-84) x ABG76561 (1-123)

Qy   1 CGGGCGAGT--- 9
          |||||||||
Db   25 ArgAlaSerGlyTyrSerPheSerLeuPheTrpValAlaTrpValArgGlnMetProGly 44

Qy   10 CAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCACATACAGC 69
         |||:::|| :|||||:||||||||:::||||:||||||||||||||||||||||||
Db   45 GlnGlyLeu--GluTrpMetAlaIleIleTyrProGlySerAspThrThrTyrSer 63

Qy   70 CCGTCCTTCCAAGGC 84
         ||||||||:::|||
Db   64 ProSerPheGluGly 68

RESULT 2
ADR46829
ID   ADR46829 standard; protein; 411 AA.
XX
AC   ADR46829;
XX
DT   18-NOV-2004   (first entry)
XX
DE   Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.
XX
KW   molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW   antigen presenting cell; APC; human; beta chorionic gonadotropin;
KW   betahCG; beta chorionic gonadotropin; antibody;
KW   T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW   immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW   CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW   melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW   antibody B11; pB11-betahCG molecular conjugate; fusion protein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200407432-A2.
XX
PD   02-SEP-2004.
XX
PF   30-JAN-2004; 2004WO-US002725.
XX
PR   31-JAN-2003; 2003US-0443979P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T, Endres M, He L, Ramakrishna V;
XX
DR   WPI; 2004-635555/61.
DR   N-PSDB; ADR46828.
XX
PT   New molecular conjugate having a monoclonal antibody that binds to human
PT   APCs linked to a beta human chorionic gonadotropin, useful for inducing a

CC   cytotoxic T cell response in cancers and infectious diseases.
PT
XX
PS   Claim 16; SEQ ID NO 12; 82pp; English.
XX
CC   The present invention describes a molecular conjugate comprising a
CC   monoclonal antibody that binds to human antigen presenting cells (APCs)
CC   linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC   comprises a heavy and/or light chain variable region derived from a human
CC   VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC   of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC   described: (1) a molecular conjugate comprising a human antibody heavy
CC   chain and a human antibody light chain, where either or both chains are
CC   linked to betahCG; (2) a molecular conjugate comprising a human single
CC   chain antibody that binds to human APCs linked to betahCG, where the
CC   conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC   (ADR46829); (3) a composition comprising any of the molecular conjugates
CC   as described above, and a carrier, optionally in combination with an
CC   adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC   against betahCG, comprising contacting any of the molecular conjugates
CC   described above with APCs such that the antigen is processed and
CC   presented to T cells in a manner which induces or enhances a T cell-
CC   mediated response against the antigen; (5) immunising a subject
CC   comprising administering any of the molecular conjugates described above,
CC   optionally in combination with an adjuvant, a cytokine which stimulates
CC   proliferation of dendritic cells and/or an immunostimulatory agent; and
CC   (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC   comprising forming a conjugate of the antigen and a monoclonal antibody
CC   which binds to APCs, and contacting the conjugate either in vivo or ex
CC   vivo with APCs such that the antigen is internalised, processed and
CC   presented to T cells in a manner which induces or enhances a cytotoxic T
CC   cell response against the antigen. The molecular conjugate has
CC   cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC   virucide and antimalarial activities, and can be used as a CD8 agonist,
CC   and in vaccines. The methods and compositions of the present invention
CC   are useful for inducing a cytotoxic T cell response, and in particular
CC   for treating autoimmune disorders, cancers and infectious diseases by
CC   eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC   including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC   herpes. The present sequence represents a human pB11-betahCG molecular
CC   conjugate, which is used in the exemplification of the present invention.
XX
SQ   Sequence 411 AA;

Alignment Scores:
Pred. No.:   0.000163   Length: 411
Score: 113.30   Matches: 26
Percent Similarity: 15.76%   Conservative: 0
Best Local Similarity: 15.76%   Mismatches: 2
Query Match: 76.55%   Indels: 137
DB: Gaps: 8

NOLAN463-2B.SEQ (1-84) x ADR46829 (1-411)

Qy   1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCC----------------------- 33
          |||||||||||||||||||||||||||||||| |||||||
Db   43 ArgAlaSerGlnGlyIleSerArgTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAla 62

Qy   33 --- 33

Db   63 ProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer 82

Qy   33 --- 33

Db   83 GlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnProGluAspPhe 102

Qy   33 --- 33

Db   103 AlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProArgThrPheGlyGlnGlyThrLys 122

Qy   33 --- 33

Db   123 ValGluIleLysGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlySerGluGlu 142

```
Qy    33 -------------------------------------------------------- 33

Db   143 ValGlnLeuValGlnSerGlyAlaGluValLysProGlySerLeuArgIleSer 162

Qy    33 -------------------------------------------------------- 33

Db   163 CysLysGlySerGlyAspSerPheThrTyrTrpIleGlyTrpValArgGlnMetPro 182

Qy    34 ----------------ATCATCTATCCTGGTGACTCTGATACCACATACAGC 69
                       |||||||||||||||||||||
Db   183 GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrIleTyrSer 202

Qy    70 CCGTCCTTCCAAGGC 84
         |||||||||||||||
Db   203 ProSerPheGlnGly 207
```

RESULT 3
AAU02582
ID   AAU02582 standard; protein; 122 AA.
XX
AC   AAU02582;
XX
DT   29-AUG-2001 (first entry)
XX
DE   Anti-adipocyte monoclonal antibody heavy chain, FAT 69.
XX
KW   Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW   heart disease; complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   WO20012779-A1.
XX
PD   19-APR-2001.
XX
PF   11-OCT-2000; 2000WO-GB003900.
XX
PR   12-OCT-1999; 99US-0158812P.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Edwards BM, Main SH, Vaughan TJ;
XX
DR   WPI; 2001-282031/29.
DR   N-PSDB; AAS03482.
XX
PT   Panel of specific binding members of antibody molecules which bind to
PT   whole adipocytes is used in the treatment of obesity and obesity related
PT   diseases.
XX
PS   Claim 1; Page 144; 182pp; English.
XX
CC   AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC   sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC   and heavy chain complementarity determining regions (CDR) of the
CC   invention. The antibodies can be used in the treatment of obesity and
CC   obesity related diseases. The antibodies can be used to deliver drugs or
CC   pro-drugs directly to the fat mass of an obese patient or the antibody
CC   can be used as a therapeutic itself. Antibodies binding specifically to
CC   adipocytes can be used to activate the immune system to destroy the cells
CC   by complement mediated lysis. The antibodies may be labeled with a
CC   detectable label such as radiolabel, fluorescent or chemical group and
CC   used in methods of diagnosis in human subjects e.g. to determine the
CC   presence of adipocyte antigen on the surface of an adipocyte to detect or
CC   determine the presence or level of adipocytes in a cell or tissue sample.
CC   The antibodies can be used as an alternative means of treatment for obese
CC   patients other than undergoing surgery to remove excess fat. Antibodies
CC   for different types of fat deposits can also be produced e.g. intra-
CC   abdominal fat associated with heart disease
XX
SQ   Sequence 122 AA;

Alignment Scores:

```
Pred. No.:                        0.000801
Score:                            106.20
Percent Similarity:               66.67%
Best Local Similarity:            60.61%
Query Match:                      71.76%
DB:                               4
```

```
Length:          122
Matches:          20
Conservative:      2
Mismatches:        3
Indels:            8
Gaps:              0
```

NOLAN463-2B.SEQ (1-84) x AAU02582 (1-122)

```
Qy     2 GGGCAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCATCCTGGTGACTCTGATACCA 61
         ||||||     |||::|    ||.:::       ||||||||||||||||||||||||
Db    42 GlyArg-----GluLeu--GluTrpMetGlyIleIleTyrProGlyAspSerAspThrA 59

Qy    62 CATACAGCCCGTCCTTCCAAGGC 84
         |||||||||||||||||||||
Db    59 rgTyrSerProSerPheGlnGly 66
```

RESULT 4
AAU14177
ID   AAU14177 standard; protein; 474 AA.
XX
AC   AAU14177;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human novel protein #48.
XX
KW   Human; novel protein; Antianaemic; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002623.
XX
PR   25-JAN-2000; 2000US-00491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22482.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage.
XX
PS   Example 4; Page 554-555; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human proteins or
CC   their active domains. The polypeptides, polynucleotides and antibodies
CC   raised against the polypeptides are used in a method of treatment of a
CC   mammal and prevention of disorders caused by the aberrant protein
CC   expression or activity. The polypeptides can be used as molecular weight
CC   markers, food supplements, and in antibody production. The polypeptides
CC   are used to identify compounds which bind to the polypeptides.
CC   Polynucleotides of the invention are used as probes and primers, for
CC   sequencing, for chromosome or gene mapping, in the production of
CC   recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC   therapy. Polypeptides of the invention can be used to target drugs to a
CC   tumour, in assays to determine biological activity, to raise
CC   antibodies/elicit an immune response, to determine quantitative protein
CC   levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,

```
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC   versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC   diseases, nervous system disorders, and infection. The present sequence
CC   represents a protein of the invention
XX
SQ   Sequence 474 AA;

Alignment Scores:
Pred. No.:             0.00199      Length:          474
Score:               104.40         Matches:          23
Percent Similarity:   47.17%        Conservative:      2
Best Local Similarity: 43.40%       Mismatches:        2
Query Match:          70.54%        Indels:           26
DB:                    4            Gaps:              2

NOLAN463-2B.SEQ (1-84) x AAU14177 (1-474)

Qy    3 GGCGAGTCA------------------------GGGTATTAGC------------------ 21
          |||||||||                        ||||| |||
Db   34 GlyGluSerValIleSerCysLysGlySerGlyTyr-SerPheSerAspTyrTrpVa 53

Qy   22 ------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                        ::|||||||| |||||||||
Db   53 lAlaTrpValArgGlnSerProAspLysGlyLeuAlaTrpMetGlyIleIleTyrProGl 73

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          |||||||||||||||||||||||||||||||||||||
Db   73 yAspSerAspThrArgTyrSerProSerPheGlnGly 85

RESULT 5
AAW54008
ID   AAW54008 standard; protein; 98 AA.
XX
AC   AAW54008;
XX
DT   25-MAR-2003  (revised)
DT   29-JUL-1998  (first entry)
XX
DE   Human Anti-CD4 antibody VH5 consensus sequence.
XX
KW   Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
KW   Old World monkey; constant domain; eczema; immuno-modulated disease;
KW   rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   US5750105-A.
XX
PD   12-MAY-1998.
XX
PF   07-JUN-1995;  95US-00476349.
XX
PR   25-JUL-1991;  91US-00735064.
PR   23-MAR-1992;  92US-00856281.
PR   10-JUL-1992;  92US-00912292.
PR   25-JAN-1995;  95US-00379072.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Raab RW, Newman RA, Hanna N;
XX
DR   WPI; 1998-296690/26.
XX
PT   Improved method for antibody treatment - uses an antibody comprising an
PT   Old World monkey variable region and a human constant domain.
XX
PS   Example 1; Fig 9e; 84pp; English.
XX
```

```
CC   This sequence is the consensus VH5 domain of an anti-CD4 antibody (Ab).
CC   This sequence can be used in the method of the invention for treating a
CC   subject, where the treatment comprises administration of an Ab. The
CC   method comprises the administration of an antibody which has an Old World
CC   monkey (e.g. baboon or macaque) variable region which binds to an antigen
CC   (Ag) (or Ag binding portion), and a human constant domain. The method is
CC   useful for the treatment of eczema and immuno-modulated diseases and
CC   especially rheumatoid arthritis. The recombinant antibodies used are
CC   sufficiently different from native monkey antibodies to allow human
CC   antigens to raise these antibodies, but similar enough to human antibody
CC   so there is no immune response to the antibodies in humans. Compared to
CC   antibodies used in therapy in prior art, these antibodies do not induce
CC   human anti-antibodies on repeated administration. They also have longer
CC   half-lives and do not have a lack of effector function with human cells.
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 98 AA;

Alignment Scores:
Pred. No.:             0.00163      Length:           98
Score:               103.40         Matches:          23
Percent Similarity:   45.28%        Conservative:      1
Best Local Similarity: 43.40%       Mismatches:        3
Query Match:          69.86%        Indels:           26
DB:                    2            Gaps:              2

NOLAN463-2B.SEQ (1-84) x AAW54008 (1-98)

Qy    3 GGCGAGTCA------------------------GGGTATTAGC------------------ 21
          |||||||||                        |||||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                        ||:::|||||||| |||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          |||||||||||||||||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 6
ABG78233
ID   ABG78233 standard; protein; 98 AA.
XX
AC   ABG78233;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human Fv molecule hypervariable region related peptide #108.
XX
KW   Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW   disulfide Fv; scFv; dsFv; cancer; carcinoma; leukaemia; adenoma;
KW   lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200259264-A2.
XX
PD   01-AUG-2002.
XX
PF   31-DEC-2001; 2001WO-US049440.
XX
PR   29-DEC-2000; 2000US-00751181.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI   Plaksin D, Peretz T;
XX
DR   WPI; 2002-619166/66.
XX
PT   Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT   or fragment, or construct of fragment with enhanced binding
```

PT   characteristics so as to selectively bind target cell in favor of other
PT   cells.
XX
PS   Claim 13; Page 205; 232pp; English.
XX
CC   The invention relates to a peptide or polypeptide comprising an Fv
CC   molecule, a construct or fragments or a construct of a fragment with
CC   enhanced binding characteristics which selectively and/or specifically
CC   binds to a target cell in favour of other cells, where binding is
CC   primarily determined by a first hypervariable region and Fv is a single
CC   chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC   association with or attached, coupled, combined, linked or fused to a
CC   pharmaceutical agent, is useful in the manufacture of a medicament, where
CC   the medicament has activity against a diseased cell, preferably a cancer
CC   cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC   myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC   acute myeloid leukaemia cell. The peptide is also useful for preparing a
CC   composition for use in inhibiting the growth of a diseased or cancer
CC   cell. This sequence represents a human Fv molecule hypervariable region
CC   related peptide of the invention
XX
SQ   Sequence 98 AA;

```
Alignment Scores:
Pred. No.:              0.00163        Length:        98
Score:                  103.40         Matches:       23
Percent Similarity:     45.28%         Conservative:  1
Best Local Similarity:  43.40%         Mismatches:    3
Query Match:            69.86%         Indels:        26
DB:                     5              Gaps:          2

NOLAN463-2B.SEQ (1-84) x ABG78233 (1-98)

Qy      3 GGGGAGTCA----------------------------GGGTATTAGC-------------- 21
          ||||||||                              ||||| |||
Db     15 GlyGluSerLeuLysLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy     22 --------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                          ||:::   |||||||||||||||
Db     34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy     48 TGACTCTGATACCACCATACAGACCCCGTCCTTCCAAGGC 84
          |||||||||||  ||||||||||||||||||||||
Db     54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 7
ABG78231
ID   ABG78231 standard; protein; 98 AA.
XX
AC   ABG78231;
XX
DT   15-NOV-2002 (first entry)
XX
DE   Human Fv molecule hypervariable region related peptide #106.
XX
KW   Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW   disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW   lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200259264-A2.
XX
PD   01-AUG-2002.
XX
PF   31-DEC-2001; 2001WO-US049440.
XX
PR   29-DEC-2000; 2000US-00751181.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI   Plaksin D, Peretz T;

XX
DR   WPI; 2002-619166/66.
XX
PT   Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT   or fragment, or construct of fragment with enhanced binding
PT   characteristics so as to selectively bind target cell in favor of other
PT   cells.
XX
PS   Claim 13; Page 204; 232pp; English.
XX
CC   The invention relates to a peptide or polypeptide comprising an Fv
CC   molecule, a construct or fragments or a construct of a fragment with
CC   enhanced binding characteristics which selectively and/or specifically
CC   binds to a target cell in favour of other cells, where binding is
CC   primarily determined by a first hypervariable region and Fv is a single
CC   chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC   association with or attached, coupled, combined, linked or fused to a
CC   pharmaceutical agent, is useful in the manufacture of a medicament, where
CC   the medicament has activity against a diseased cell, preferably a cancer
CC   cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC   myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC   acute myeloid leukaemia cell. The peptide is also useful for preparing a
CC   composition for use in inhibiting the growth of a diseased or cancer
CC   cell. This sequence represents a human Fv molecule hypervariable region
CC   related peptide of the invention
XX
SQ   Sequence 98 AA;

```
Alignment Scores:
Pred. No.:              0.00163        Length:        98
Score:                  103.40         Matches:       23
Percent Similarity:     45.28%         Conservative:  1
Best Local Similarity:  43.40%         Mismatches:    26
Query Match:            69.86%         Indels:        2
DB:                     5              Gaps:          2

NOLAN463-2B.SEQ (1-84) x ABG78231 (1-98)

Qy      3 GGGGAGTCA----------------------------GGGTATTAGC-------------- 21
          ||||||||                              ||||| |||
Db     15 GlyGluSerLeuLysLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy     22 --------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                          ||:::   |||||||||||||||
Db     34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy     48 TGACTCTGATACCACCATACAGACCCCGTCCTTCCAAGGC 84
          |||||||||||  ||||||||||||||||||||||
Db     54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 8
ABG78232
ID   ABG78232 standard; protein; 98 AA.
XX
AC   ABG78232;
XX
DT   15-NOV-2002 (first entry)
XX
DE   Human Fv molecule hypervariable region related peptide #107.
XX
KW   Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW   disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW   lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200259264-A2.
XX
PD   01-AUG-2002.
XX
PF   31-DEC-2001; 2001WO-US049440.
XX
PR   29-DEC-2000; 2000US-00751181.

XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI Plaksin D, Peretz T;
XX
DR WPI; 2002-619166/66.
XX
PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS Claim 13; Page 204-205; 232pp; English.
XX
CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 98 AA;

Alignment Scores:
Pred. No.:   0.00163   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 5   Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABG78232 (1-98)

Qy   3 GGGGAGTCA------------------GGGTATTAGC------------- 21
         |||||||| |||||||| |||
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy 22 -----------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                      ||||:::: ||||||||||||||
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy 48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         |||||||||||||||||||||||||||||||||||||
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 9
ABG91924
ID ABG91924 standard; protein; 98 AA.
XX
AC ABG91924;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #108.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX

PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 281; 0pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX
SQ Sequence 98 AA;

Alignment Scores:
Pred. No.:   0.00163   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 5   Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABG91924 (1-98)

Qy   3 GGGGAGTCA------------------GGGTATTAGC------------- 21
         |||||||| |||||||| |||
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy 22 -----------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                      ||||:::: ||||||||||||||
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy 48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         |||||||||||||||||||||||||||||||||||||
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 10
ABG91922
ID ABG91922 standard; protein; 98 AA.
XX

```
AC   ABG91922;
XX
DT   04-DEC-2002 (first entry)
XX
DE   Human antibody fragment #106.
XX
KW   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW   metastasis; hypervariable region; autoimmune disease; thrombosis;
KW   restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW   myocardial infarction; retinopathic disease; abnormal platelet function;
KW   sulphated tyrosine-dependent protein-protein interaction.
XX
OS   Homo sapiens.
XX
PN   WO200253700-A2.
XX
PD   11-JUL-2002.
XX
PF   31-DEC-2001; 2001WO-US049442.
XX
PR   29-DEC-2000; 2000US-00751181.
PR   29-DEC-2000; 2000US-0258948P.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A,   Mar-Haim H;
PI   Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR   WPI; 2002-674776/72.
XX
PT   Novel isolated epitope present on cancer cells and important in
PT   physiological phenomena such as cell rolling, metastasis and
PT   inflammation, for treating autoimmune, inflammatory or cardiovascular
PT   diseases, and cancer.
XX
PS   Disclosure; Page 280; 0pp; English.
XX
CC   The invention relates to an isolated epitope present on cancer cells and
CC   important in physiological phenomena such as cell rolling, metastasis and
CC   inflammation, where the epitope is capable of being bound by an antibody,
CC   its antigen-binding fragment or its complex comprising at least one
CC   antibody or its binding fragment having a first hypervariable region. The
CC   epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC   disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC   tumour or leukaemia cells, increase in number of tumour or leukaemia
CC   cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC   platelet and/or cell-platelet adhesion or aggregation, for increasing
CC   mortality of tumour or leukaemia cells, for increasing the susceptibility
CC   of diseased cells to damage by anti-disease, anti-cancer or anti-
CC   leukaemia agents, or for decreasing the number of tumour or leukaemia
CC   cells in a patient, or in the manufacture of a medicament for the above
CC   mentioned purposes. The epitopes are useful for diagnosing and treating
CC   diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC   diseases, cardiovascular diseases such as myocardial infarction,
CC   retinopathic diseases and other diseases mediated by abnormal platelet
CC   function and diseases caused by sulphated tyrosine-dependent protein-
CC   protein interactions. This sequence represents a human antibody fragment
CC   of the invention
XX
SQ   Sequence 98 AA;

Alignment Scores:
Pred. No.:              0.00163          Length:          98
Score:                 103.40           Matches:         23
Percent Similarity:    45.28%           Conservative:    1
Best Local Similarity: 43.40%           Mismatches:      3
Query Match:           69.86%           Indels:          26
DB:                    5                Gaps:            2

NOLAN463-2B.SEQ (1-84) x ABG91922 (1-98)

Qy       3 GGCGAGTCA-------------------GGGTATTAGC----------- 21
           |||||||||                       |||||| |||


Db      15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
Qy      22 ------------------------------AGCTGGTTAGCCATCATCATCCTGG 47
           |||:::
Db      34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
Qy      48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
           ||||||||||||   ||||||||||||||
Db      54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 11
ABG91923
ID   ABG91923 standard; protein; 98 AA.
XX
AC   ABG91923;
XX
DT   04-DEC-2002 (first entry)
XX
DE   Human antibody fragment #107.
XX
KW   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW   metastasis; hypervariable region; autoimmune disease; thrombosis;
KW   restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW   myocardial infarction; retinopathic disease; abnormal platelet function;
KW   sulphated tyrosine-dependent protein-protein interaction.
XX
OS   Homo sapiens.
XX
PN   WO200253700-A2.
XX
PD   11-JUL-2002.
XX
PF   31-DEC-2001; 2001WO-US049442.
XX
PR   29-DEC-2000; 2000US-00751181.
PR   29-DEC-2000; 2000US-0258948P.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A,   Mar-Haim H;
PI   Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR   WPI; 2002-674776/72.
XX
PT   Novel isolated epitope present on cancer cells and important in
PT   physiological phenomena such as cell rolling, metastasis and
PT   inflammation, for treating autoimmune, inflammatory or cardiovascular
PT   diseases, and cancer.
XX
PS   Disclosure; Page 280-281; 0pp; English.
XX
CC   The invention relates to an isolated epitope present on cancer cells and
CC   important in physiological phenomena such as cell rolling, metastasis and
CC   inflammation, where the epitope is capable of being bound by an antibody,
CC   its antigen-binding fragment or its complex comprising at least one
CC   antibody or its binding fragment having a first hypervariable region. The
CC   epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC   disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC   tumour or leukaemia cells, increase in number of tumour or leukaemia
CC   cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC   platelet and/or cell-platelet adhesion or aggregation, for increasing
CC   mortality of tumour or leukaemia cells, for increasing the susceptibility
CC   of diseased cells to damage by anti-disease, anti-cancer or anti-
CC   leukaemia agents, or for decreasing the number of tumour or leukaemia
CC   cells in a patient, or in the manufacture of a medicament for the above
CC   mentioned purposes. The epitopes are useful for diagnosing and treating
CC   diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC   diseases, cardiovascular diseases such as myocardial infarction,
CC   retinopathic diseases and other diseases mediated by abnormal platelet
CC   function and diseases caused by sulphated tyrosine-dependent protein-
CC   protein interactions. This sequence represents a human antibody fragment
CC   of the invention
XX
```

SQ   Sequence 98 AA;

```
Alignment Scores:
Pred. No.:              0.00163          Length:          98
Score:                  103.40           Matches:         23
Percent Similarity:     45.28%           Conservative:    1
Best Local Similarity:  43.40%           Mismatches:      3
Query Match:            69.86%           Indels:          26
DB:                                       Gaps:           2

NOLAN463-2B.SEQ (1-84) x ABG91923 (1-98)

Qy    3 GGGCAGTCA--------------------------GGGTATTAGC----------------- 21
         ||||||||                           ||||||||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 --------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                    ||||:::  ||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         |||||||||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 12
ABU56809
ID   ABU56809 standard; protein; 98 AA.
XX
AC   ABU56809;
XX
DT   03-APR-2003 (first entry)
XX
DE   Human Immunglobulin heavy variable chain polypeptide #5.
XX
KW   Human; tumour; cancer; systemic lupus erythematosus;
KW   immunoglobulin constant region; immunoglobulin variable region;
KW   autoimmune response; rheumatoid arthritis; eczema; lymphoma;
KW   immunomodulatory disease; leukaemia; Hashimoto's thyroiditis;
KW   autoimmune carditis; Addison's disease; type I-diabetes mellitus;
KW   multiple sclerosis; male infertility; autoimmune hemolytic anaemia;
KW   inflammatory bowel disease; Sjogren's syndrome; psoriasis.
XX
OS   Homo sapiens.
XX
PN   US2002150580-A1.
XX
PD   17-OCT-2002.
XX
PF   08-MAY-2001; 2001US-00850165.
XX
PR   25-JUL-1991; 91US-00735064.
PR   23-MAR-1992; 92US-00856281.
PR   10-JUL-1992; 92US-00912292.
PR   25-JAN-1995; 95US-00379072.
PR   07-JUN-1995; 95US-00476237.
PR   21-MAY-1998; 98US-00082472.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Newman RA, Hanna N, Raab RW;
XX
DR   WPI; 2003-182483/18.
XX
PT   New recombinant chimeric antibodies comprising human, chimpanzee and Old
PT   World monkey portions, useful for treating e.g. cancer, eczema, leukemia,
PT   lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male
PT   infertility.
XX
PS   Disclosure; Fig 9E; 101pp; English.
XX
CC   The invention describes a recombinant antibody comprising a human,
CC   chimpanzee or a first Old World monkey immunoglobulin constant region,
CC   and an antigen-binding portion of a second Old World monkey

CC   immunoglobulin variable region. The first and second Old World monkey can
CC   be the same or different. The recombinant antibody is useful for treating
CC   a human having the antigen described above, e.g. for treating cancer in a
CC   human having a tumour antigen, or for treating a human suffering from an
CC   autoimmune response (where the antigen is involved in an autoimmune
CC   response in the human). In particular, the recombinant antibody is useful
CC   for treating rheumatoid arthritis, eczema, or an immunomodulatory
CC   disease. The recombinant antibody is also useful for treating tumours,
CC   leukaemia, lymphoma, Hashimoto's thyroiditis, autoimmune carditis,
CC   Addison's disease, type I-diabetes mellitus, multiple sclerosis, male
CC   infertility, autoimmune hemolytic anaemia, inflammatory bowel disease,
CC   Sjogren's syndrome, psoriasis, or systemic lupus erythematosus. This is
CC   the amino acid sequence of a human immunoglobulin heavy variable chain
CC   polypeptide for creation of the recombinant antibody
XX
SQ   Sequence 98 AA;

```
Alignment Scores:
Pred. No.:              0.00163          Length:          98
Score:                  103.40           Matches:         23
Percent Similarity:     45.28%           Conservative:    1
Best Local Similarity:  43.40%           Mismatches:      3
Query Match:            69.86%           Indels:          26
DB:                                       Gaps:           2

NOLAN463-2B.SEQ (1-84) x ABU56809 (1-98)

Qy    3 GGGCAGTCA--------------------------GGGTATTAGC----------------- 21
         ||||||||                           ||||||||
Db   15 GlyGluSerLeu***IleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 --------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                    ||||:::  ||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCAGCCCGTCCTTCCAAGGC 84
         |||||||||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 13
ABP56508
ID   ABP56508 standard; protein; 98 AA.
XX
AC   ABP56508;
XX
DT   20-MAR-2003 (first entry)
XX
DE   Human anti-Fc-epsilon-R1 alpha autoantibody heavy chain VHVCW.
XX
KW   Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive;
KW   allergic disease; urticaria; late phase allergic reaction; malignancy;
KW   intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E;
KW   conditional autoimmunity; IgE mediated disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO20028205-A2.
XX
PD   17-OCT-2002.
XX
PF   03-APR-2002; 2002WO-EP003660.
XX
PR   04-APR-2001; 2001US-0281024P.
XX
PA   (ZLBB-) ZLB BIOPLASMA AG.
XX
PI   Miescher S;
XX
DR   WPI; 2003-103348/09.
XX
PT   Identifying and obtaining inhibitor of a pathological process for
PT   treating e.g. autoimmunity comprises determining if a compound is capable

```
PT    of modulating the binding of the Fc-epsilon-R1 receptor and an
PT    autoantibody against its alpha-chain.
XX
PS    Claim 20; Page 22; 29pp; English.
XX
CC    The present invention describes a method for identifying and obtaining an
CC    inhibitor of a pathological process. The method comprises determining if
CC    a compound is capable of modulating the binding of the Fc-epsilon-R1
CC    receptor alpha-chain and an autoantibody against its alpha-chain. Also
CC    described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor
CC    alpha-chain for identifying and obtaining an inhibitor of a pathological
CC    process; (2) use of the identified inhibitor for inhibiting activity of
CC    the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and (3)
CC    a compound identified by the method, which binds but does not activate
CC    the receptor; and (4) a polypeptide capable of specific binding to the Fc
CC    -epsilon-R1 receptor alpha-chain. The method is useful for obtaining an
CC    inhibitor of a pathological process e.g. imbalance between cell-bound and
CC    free IgE e.g. allergic disease (urticaria, late phase allergic reactions,
CC    intrinsic asthma, drug intolerance and food intolerance), IgE mediated
CC    disease or malignancy. The compound is useful for treating a pathological
CC    process, particularly conditional autoimmunity. The present sequence
CC    represents a human recombinant anti-Fc-epsilon-R1 alpha autoantibody
CC    heavy chain protein sequence from the present invention
XX
SQ    Sequence 98 AA;

Alignment Scores:
Pred. No.:                         98
Score:                0.00163   Length:          98
Percent Similarity:   103.40    Matches:         23
Best Local Similarity: 45.28%   Conservative:     1
Query Match:          43.40%    Mismatches:       3
                      69.86%    Indels:          26
DB:                             Gaps:             2

NOLAN463-2B.SEQ (1-84) x ABP56508 (1-98)

Qy    3  GGCGAGTCA--------------------------GGGTATTAGC------------------- 21
         |||||||||                          ||||||||||
Db   15  GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIle 34

Qy   22  ---------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                               ||||:::   ||||||||||||||||
Db   34  eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48  TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         ||||||||||||   ||||||||||||||||||
Db   54  yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 14
ABJ18687
ID    ABJ18687 standard; protein; 98 AA.
XX
AC    ABJ18687;
XX
DT    06-MAR-2003  (first entry)
XX
DE    Antibody library related human protein sequence SEQ ID No 16.
XX
KW    Library; recombinant antibody; clustering variable region; in silico;
KW    immunogenecity; antibody therapeutic; human.
XX
OS    Homo sapiens.
XX
PN    WO200284277-A1.
XX
PD    24-OCT-2002.
XX
PF    17-APR-2002; 2002WO-US012202.
XX
PR    17-APR-2001; 2001US-0284407P.
XX
PA    (ABMA-) ABMAXIS INC.
XX
```

```
PI    Luo P;
XX
DR    WPI; 2003-093043/08.
XX
PT    Constructing a library of recombinant antibodies useful as source of
PT    antibody candidates for screening antigens comprises clustering variable
PT    regions of antibodies having known 3-dimensional structures into
PT    structural ensembles.
XX
PS    Disclosure; Page 109-110; 119pp; English.
XX
CC    The invention relates to a novel method for the construction of a library
CC    of recombinant antibodies. The novel method comprises clustering variable
CC    regions of a collection of antibodies having known 3D structures into at
CC    least two families of structural ensembles, each comprising at least two
CC    different antibody sequences but with substantially identical main chain
CC    conformations. The method is useful for constructing a library of
CC    artificial antibodies in silico which provides a structurally diverse and
CC    yet functionally more relevant source of antibody candidates which can
CC    then be screened for binding a wide variety of target molecules,
CC    including small molecules, and biomacromolecules such as proteins,
CC    peptides and nucleic acids. The libraries constructed are useful as a
CC    source of affinity candidates for further screening for novel antibodies
CC    with high affinity against a wide range of antigens and having no or
CC    minimum immunogenecity to human subjects treated with antibody
CC    therapeutics. This sequence represents a human peptide region of an
CC    antibody relating to the novel antibody library construction method of
CC    the invention
XX
SQ    Sequence 98 AA;

Alignment Scores:
Pred. No.:                         98
Score:                0.00163   Length:          98
Percent Similarity:   103.40    Matches:         23
Best Local Similarity: 45.28%   Conservative:     1
Query Match:          43.40%    Mismatches:       3
                      69.86%    Indels:          26
DB:                             Gaps:             2

NOLAN463-2B.SEQ (1-84) x ABJ18687 (1-98)

Qy    3  GGCGAGTCA--------------------------GGGTATTAGC 21
         ||||||||||                          ||||||||||
Db   15  GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIle 34

Qy   22  ---------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                               ||:::    ||||||||||||
Db   34  eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48  TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         |||||||||||||   |||||||||||||||||
Db   54  yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 15
ABO27112
ID    ABO27112 standard; protein; 98 AA.
XX
AC    ABO27112;
XX
DT    10-SEP-2003  (first entry)
XX
DE    Human germline heavy chain variable region gene segment #45.
XX
KW    Human; heavy chain variable region; VH; humanised antibody;
KW    chimeric antibody; complementarity determining region; CDR;
KW    canonical CDR structure type.
XX
OS    Homo sapiens.
XX
PN    US200303649-A1.
XX
PD    27-FEB-2003.
XX
```

PF   12-JUL-2002; 2002US-00194975.
XX
PR   12-JUL-2001; 2001US-0305111P.
XX
PA   (FOOT/) FOOTE J.
XX
PI   Foote J;
XX
DR   WPI; 2003-492151/46.
XX
PT   Making humanized antibody for converting antibody, by making chimeric
PT   antibodies containing complementarity determining region from non-human
PT   antibody and appropriate framework sequences of human antibodies.
XX
PS   Example 1; Fig 1; 31pp; English.
XX
CC   The invention describes a method of making a humanised antibody,
CC   comprising making chimeric antibodies containing a complementarity
CC   determining region (CDR) from a non-human antibody and appropriate
CC   framework sequences (I) of human antibodies. (I) is selected by using
CC   canonical CDR structure types of non-human antibody in comparison to
CC   germline canonical CDR structure types of human antibodies as the basis
CC   for selection, for humanisation. The method is useful for making a
CC   humanised antibody or a converted antibody. The method is applicable for
CC   converting a subject antibody sequence of any subject species to a less
CC   immunogenic form suitable for use in an object species. The method is
CC   reliable for identifying suitable human framework sequences to support
CC   non-human CDR regions and to provide humanised antibodies that retain
CC   high antigen binding with low immunogenicity in humans, without the need
CC   for direct comparison of framework sequences, without the need for
CC   determining critically important amino acid residues in the framework,
CC   and without the need for multiple iteration and construction to obtain
CC   humanised antibodies with suitable therapeutic properties. The antibody
CC   has high affinity and low immunogenicity without need for comparing
CC   framework sequences between non-human and human antibodies. This sequence
CC   represents a human heavy chain variable region gene segment used in the
CC   creation of humanised antibodies
XX
SQ   Sequence 98 AA;

Alignment Scores:
Pred. No.:   0.00163   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 6   Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABO27112 (1-98)

Qy   3 GGCGAGTCA------------------GGGTATTAGC--------------- 21
           |||||||| |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                         |||::: |||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
           ||||||||| ||||||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

Search completed: August 4, 2005, 18:55:57
Job time : 93 secs

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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August 4, 2005, 18:44:26 ; Search time 22.25 Seconds
                                       (without alignments)
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Perfect score:  148
Sequence:       1 CGGGCGAGTCAGGTATTAG.........ACAGCCCGTCCTTCCAAGGC 84

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                Fgapop   6.0 , Fgapext   0.1
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Searched:       513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:      1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	103.4	69.9	98	1	US-08-478-039-81	Sequence 81, Appl
2	103.4	69.9	98	1	US-08-476-349A-81	Sequence 81, Appl
3	103.4	69.9	98	2	US-08-665-202-33	Sequence 33, Appl
4	103.4	69.9	98	4	US-09-315-574-33	Sequence 33, Appl
5	103.4	69.9	117	3	US-08-545-809A-133	Sequence 133, App
6	103.4	69.9	119	3	US-09-025-769B-26	Sequence 26, Appl
7	103.4	69.9	119	4	US-09-490-070A-26	Sequence 26, Appl
8	103.4	69.9	119	4	US-09-490-153-26	Sequence 26, Appl
9	103.4	69.9	119	4	US-09-490-324-26	Sequence 26, Appl
10	103.4	69.9	120	3	US-09-025-769B-40	Sequence 40, Appl
11	103.4	69.9	120	3	US-09-025-769F-67	Sequence 67, Appl
12	103.4	69.9	120	4	US-09-490-070A-40	Sequence 40, Appl
13	103.4	69.9	120	4	US-09-490-070A-67	Sequence 67, Appl
14	103.4	69.9	120	4	US-09-490-153-40	Sequence 40, Appl
15	103.4	69.9	120	4	US-09-490-153-67	Sequence 67, Appl
16	103.4	69.9	120	4	US-09-490-324-40	Sequence 40, Appl
17	103.4	69.9	120	4	US-09-490-324-67	Sequence 67, Appl
18	103.2	69.7	111	4	US-09-726-219A-171	Sequence 171, App
19	98.2	66.4	122	3	US-08-983-607-30	Sequence 30, Appl
20	95	64.2	125	2	US-08-665-202-44	Sequence 44, Appl
21	95	64.2	125	4	US-09-315-574-44	Sequence 44, Appl
22	95	64.2	129	2	US-08-665-202-32	Sequence 32, Appl
23	95	64.2	129	4	US-09-315-574-32	Sequence 32, Appl
24	95	64.2	258	2	US-08-665-202-5	Sequence 5, Appl
25	95	64.2	258	4	US-09-315-574-5	Sequence 5, Appl
26	95	64.2	262	3	US-09-069-821-4	Sequence 4, Appl
27	95	64.2	262	4	US-09-956-086-4	Sequence 4, Appl
28	95	64.2	262	4	US-09-956-087-4	Sequence 4, Appl
29	95	64.2	282	3	US-09-420-592A-7	Sequence 7, Appl
30	95	64.2	282	4	US-09-985-442-7	Sequence 7, Appl
31	95	64.2	282	4	US-09-983-580-7	Sequence 7, Appl
32	93.6	63.2	125	2	US-08-665-202-48	Sequence 48, Appl
33	93.6	63.2	125	2	US-08-665-202-49	Sequence 49, Appl
34	93.6	63.2	125	2	US-08-665-202-50	Sequence 50, Appl
35	93.6	63.2	125	2	US-08-665-202-51	Sequence 51, Appl
36	93.6	63.2	125	2	US-08-665-202-52	Sequence 52, Appl
37	93.6	63.2	125	2	US-08-665-202-57	Sequence 57, Appl
38	93.6	63.2	125	4	US-09-315-574-48	Sequence 48, Appl
39	93.6	63.2	125	4	US-09-315-574-49	Sequence 49, Appl
40	93.6	63.2	125	4	US-09-315-574-50	Sequence 50, Appl
41	93.6	63.2	125	4	US-09-315-574-51	Sequence 51, Appl
42	93.6	63.2	125	4	US-09-315-574-52	Sequence 52, Appl
43	93.6	63.2	125	4	US-09-315-574-57	Sequence 57, Appl
44	93.2	63.0	88	2	US-09-726-219A-172	Sequence 172, App
45	92.9	62.8	125	2	US-08-665-202-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-478-039-81
; Sequence 81, Application US/0847803 9
Patent No. 5681722
GENERAL INFORMATION:
  APPLICANT: Newman, Roland A.
  APPLICANT: Hanna, Nabil
  APPLICANT: Raab, Ronald W.
  TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
  NUMBER OF SEQUENCES: 114
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince St.
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22313-1404
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/478,039
    FILING DATE: 07-JUN-1995
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/379,072
    FILING DATE: 25-JAN-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/912,292
    FILING DATE: 10-JUL-1992
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/856,281
    FILING DATE: 23-MAR-1992
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 consensus
US-08-478-039-81

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Alignment Scores:
Pred. No.:               0.000271      Length:          98
Score:                   103.40        Matches:         23
Percent Similarity:      45.28%        Conservative:    1
Best Local Similarity:   43.40%        Mismatches:      3
Query Match:             69.86%        Indels:          26
DB:                                    Gaps:            2

NOLAN463-2B.SEQ (1-84) x US-08-478-039-81 (1-98)

Qy    3 GGCGAGTCA------------------------GGGTATTAGC------------ 21
         ||||||||                         |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                         |||:::  ||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         |||||||||   |||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 2
US-08-476-349A-81
; Sequence 81, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH5 consensus
US-08-476-349A-81

```
Alignment Scores:
Pred. No.:               0.000271      Length:          98
Score:                   103.40        Matches:         23
Percent Similarity:      45.28%        Conservative:    1
Best Local Similarity:   43.40%        Mismatches:      3
Query Match:             69.86%        Indels:          26
DB:                                    Gaps:            2

NOLAN463-2B.SEQ (1-84) x US-08-476-349A-81 (1-98)

Qy    3 GGCGAGTCA------------------------GGGTATTAGC------------ 21
         ||||||||                         |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                         ||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         ||||||||||  |||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 3
US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/665,202
    FILING DATE: 13-JUN-1996
    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/000,238
    FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/000,250
    FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
    NAME: Hunter, Tom
    REGISTRATION NUMBER: 38,498
    REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX:   (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 98 amino acids
        TYPE: amino acid
        STRANDEDNESS:
        TOPOLOGY: linear
    MOLECULE TYPE: peptide
US-08-665-202-33

Alignment Scores:
Pred. No.:             0.000271       Length:         98
Score:                 103.40         Matches:        23
Percent Similarity:    45.28%         Conservative:   1
Best Local Similarity: 43.40%         Mismatches:     3
Query Match:           69.86%         Indels:         26
DB:                    2              Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-08-665-202-33 (1-98)

Qy    3 GGCGAGTCA----------------------GGGTATTAGC---------- 21
          |||||||||                     |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                      ||:::|||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          |||||||||| |||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 4
US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
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    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/000,238
    FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/000,250
    FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/665,202
    FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
    NAME: Hunter, Tom
    REGISTRATION NUMBER: 38,498
    REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX:   (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 98 amino acids
        TYPE: amino acid
        STRANDEDNESS:
        TOPOLOGY: linear
    MOLECULE TYPE: peptide
US-09-315-574-33

Alignment Scores:
Pred. No.:             0.000271       Length:         98
Score:                 103.40         Matches:        23
Percent Similarity:    45.28%         Conservative:   1
Best Local Similarity: 43.40%         Mismatches:     3
Query Match:           69.86%         Indels:         26
DB:                    4              Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-09-315-574-33 (1-98)

Qy    3 GGCGAGTCA----------------------GGGTATTAGC---------- 21
          |||||||||                     |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                      ||:::|||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          |||||||||| |||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 5
US-08-545-809A-133
; Sequence 133, Application US/0854809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-133

Alignment Scores:
Pred. No.:   0.00288   Length: 117
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 3   Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-08-545-809A-133 (1-117)

Qy   3 GGCGAGTCA------------------------------GGGTATTAGC------------ 21
           ||||||||| ||||| |||
Db   34 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 53

Qy   22 ------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                   |||::: |||||||||||||
Db   54 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 73

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
           |||||||||||| ||||||||||||||||||||||||
Db   73 yAspSerAspThrArgTyrSerProSerPheGlnGly 85

RESULT 6
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-26

Alignment Scores:
Pred. No.:   0.00029   Length: 119
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 3   Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-025-769B-26 (1-119)

Qy   3 GGCGAGTCA------------------------------GGGTATTAGC------------ 21
           ||||||||| ||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                   |||::: |||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
           |||||||||||| ||||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 7
US-09-490-070A-26
; Sequence 26, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005

```
        TELECOMMUNICATION INFORMATION:
           TELEPHONE: (202) 912-2000
           TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 26:
     SEQUENCE CHARACTERISTICS:
        LENGTH: 119 amino acids
        TYPE: amino acid
        STRANDEDNESS: <Unknown>
        TOPOLOGY: linear
     MOLECULE TYPE: protein
     SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

Alignment Scores:
Pred. No.:             0.00029      Length:        119
Score:                 103.40       Matches:        23
Percent Similarity:    45.28%       Conservative:    1
Best Local Similarity: 43.40%       Mismatches:      3
Query Match:           69.86%       Indels:         26
DB:                    4            Gaps:            2

NOLAN463-2B.SEQ (1-84) x US-09-490-070A-26 (1-119)

Qy  3 GGGGAGTCA------------------GGGTATTAGC------------------ 21
       ||||||||                    |||||| |||
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy 22 ---------------------AGCTGGTTAGCCATCATCATCCTGG 47
                            |||:::   ||||||||||||||
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy 48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
       |||||||||||| ||||||||||||||||||||||||
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 8
US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
     APPLICANT: Knappik, Achim
                Pack, Peter
                Ilag, Vic
                Ge, Liming
                Moroney, Simon
                Plueckthun, Andreas
     TITLE OF INVENTION: Protein/(Poly)peptide libraries
     NUMBER OF SEQUENCES: 373
     CORRESPONDENCE ADDRESS:
        ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
        STREET: 1251 Avenue of the Americas
        CITY: New York
        STATE: New York
        COUNTRY: USA
        ZIP: 10021
     COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/490,153
        FILING DATE: 24-Jan-2000
     PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/09/025,769B
        FILING DATE: 18-FEB-1998
        APPLICATION NUMBER: EP 95 11 3021.0
        FILING DATE: 18-AUG-1995
     ATTORNEY/AGENT INFORMATION:
        NAME: James F. Haley, Jr., Esq.
        REGISTRATION NUMBER: 27,794
        REFERENCE/DOCKET NUMBER: MORPHO/5
        TELECOMMUNICATION INFORMATION:
```

```
        TELEPHONE: (212)596-9000
        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
     SEQUENCE CHARACTERISTICS:
        LENGTH: 119 amino acids
        TYPE: amino acid
        STRANDEDNESS: <Unknown>
        TOPOLOGY: linear
     MOLECULE TYPE: protein
     SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

Alignment Scores:
Pred. No.:             0.00029      Length:        119
Score:                 103.40       Matches:        23
Percent Similarity:    45.28%       Conservative:    1
Best Local Similarity: 43.40%       Mismatches:      3
Query Match:           69.86%       Indels:         26
DB:                    4            Gaps:            2

NOLAN463-2B.SEQ (1-84) x US-09-490-153-26 (1-119)

Qy  3 GGGGAGTCA------------------GGGTATTAGC------------------ 21
       ||||||||                    |||||| |||
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy 22 ---------------------AGCTGGTTAGCCATCATCATCCTGG 47
                            |||:::   ||||||||||||||
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy 48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
       |||||||||||| ||||||||||||||||||||||||
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 9
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
     APPLICANT: Knappik, Achim
                Pack, Peter
                Ilag, Vic
                Ge, Liming
                Moroney, Simon
                Plueckthun, Andreas
     TITLE OF INVENTION: Protein/(Poly)peptide libraries
     NUMBER OF SEQUENCES: 373
     CORRESPONDENCE ADDRESS:
        ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
        STREET: 1251 Avenue of the Americas
        CITY: New York
        STATE: New York
        COUNTRY: USA
        ZIP: 10021
     COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/490,324
        FILING DATE: 24-Jan-2000
     PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/09/025,769
        FILING DATE: 18-FEB-1998
        APPLICATION NUMBER: EP 95 11 3021.0
        FILING DATE: 18-AUG-1995
     ATTORNEY/AGENT INFORMATION:
        NAME: James F. Haley, Jr., Esq.
        REGISTRATION NUMBER: 27,794
        REFERENCE/DOCKET NUMBER: MORPHO/5
        TELEPHONE: (212) 596-9000
```

```
;;      TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 26:
;;      SEQUENCE CHARACTERISTICS:
;;           LENGTH: 119 amino acids
;;           TYPE: amino acid
;;           STRANDEDNESS: <Unknown>
;;           TOPOLOGY: linear
;;      MOLECULE TYPE: protein
;;      SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

Alignment Scores:
Pred. No.:               0.00029          Length:          119
Score:                   103.40           Matches:         23
Percent Similarity:      45.28%           Conservative:    1
Best Local Similarity:   43.40%           Mismatches:      3
Query Match:             69.86%           Indels:          26
DB:                      4                Gaps:            2

NOLAN463-2B.SEQ (1-84) x US-09-490-324-26 (1-119)

Qy       3 GGCGAGTCA-------------------------------GGGTATTAGC--------- 21
           |||||||||                               ||||| |||
Db      15 GlyGluSerLeuIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy      22 --------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                                 |||::: ||||||||||
Db      34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 66

Qy      48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
           ||||||||||||||||||||||||||||||||||||||
Db      54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 10
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
;    APPLICANT: Knappik, Achim
;    APPLICANT: Pack, Peter
;    APPLICANT: Ilag, Vic
;    APPLICANT: Ge, Liming
;    APPLICANT: Moroney, Simon
;    APPLICANT: Plueckthun, Andreas
;    TITLE OF INVENTION: Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES: 373
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;       STREET: 1251 Avenue of the Americas
;       CITY: New York
;       STATE: New York
;       COUNTRY: USA
;       ZIP: 10021
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/025,769B
;       FILING DATE: 18-FEB-1998
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: EP 95 11 3021.0
;       FILING DATE: 18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;       NAME: James F. Haley, Jr., Esq.
;       REGISTRATION NUMBER: 27,794
;       REFERENCE/DOCKET NUMBER: MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212)596-9000
;       TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 40:
;;      SEQUENCE CHARACTERISTICS:
```

```
;;           LENGTH: 120 amino acids
;;           TYPE: amino acid
;;           STRANDEDNESS:
;;           TOPOLOGY: linear
;;      MOLECULE TYPE: protein
US-09-025-769B-40

Alignment Scores:
Pred. No.:               0.00029          Length:          120
Score:                   103.40           Matches:         23
Percent Similarity:      45.28%           Conservative:    1
Best Local Similarity:   43.40%           Mismatches:      3
Query Match:             69.86%           Indels:          26
DB:                      3                Gaps:            2

NOLAN463-2B.SEQ (1-84) x US-09-025-769B-40 (1-120)

Qy       3 GGCGAGTCA-------------------------------GGGTATTAGC--------- 21
           |||||||||                               ||||| |||
Db      15 GlyGluSerLeuIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy      22 --------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                                 |||::: ||||||||||
Db      34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 66

Qy      48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
           ||||||||||||||||||||||||||||||||||||||
Db      54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 11
US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No 6300064
; GENERAL INFORMATION:
;    APPLICANT: Knappik, Achim
;    APPLICANT: Pack, Peter
;    APPLICANT: Ilag, Vic
;    APPLICANT: Ge, Liming
;    APPLICANT: Moroney, Simon
;    APPLICANT: Plueckthun, Andreas
;    TITLE OF INVENTION: Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES: 373
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;       STREET: 1251 Avenue of the Americas
;       CITY: New York
;       STATE: New York
;       COUNTRY: USA
;       ZIP: 10021
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/025,769B
;       FILING DATE: 18-FEB-1998
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: EP 95 11 3021.0
;       FILING DATE: 18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;       NAME: James F. Haley, Jr., Esq.
;       REGISTRATION NUMBER: 27,794
;       REFERENCE/DOCKET NUMBER: MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212)596-9000
;       TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 67:
;;      SEQUENCE CHARACTERISTICS:
;;           LENGTH: 120 amino acids
;;           TYPE: amino acid
;;           TOPOLOGY: linear
;;      MOLECULE TYPE: protein
```

US-09-025-769B-67

Alignment Scores:
Pred. No.:   0.00029   Length: 120
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-025-769B-67 (1-120)

Qy   3 GGCCAGTCA--------------GGGTATTAGC------ 21
        ||||||||| ||||| |||
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy 22 -----------------AGCTGGTTAGCCATCATCTATCCTGG 47
                       ||||::: ||||||||||||
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy 48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
        |||||||||| ||||||||||||||||||
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 12
US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;   White & McAuliffe
;   STREET: 1666 K Street, N.W., Suite 300
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20006
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,070A
;   FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Colin G. Sandercock, Esq.
;   REGISTRATION NUMBER: 31,298
;   REFERENCE/DOCKET NUMBER: 37629-0005
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 912-2000
;   TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 40:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40

Alignment Scores:
Pred. No.:   0.00029   Length: 120
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-070A-40 (1-120)

Qy   3 GGCCAGTCA--------------GGGTATTAGC------ 21
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Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy 22 -----------------AGCTGGTTAGCCATCATCTATCCTGG 47
                       ||||::: ||||||||||||
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy 48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
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Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 13
US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;   White & McAuliffe
;   STREET: 1666 K Street, N.W., Suite 300
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20006
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,070A
;   FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Colin G. Sandercock, Esq.
;   REGISTRATION NUMBER: 31,298
;   REFERENCE/DOCKET NUMBER: 37629-0005
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 912-2000
;   TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 67:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

Alignment Scores:
Pred. No.:   0.00029   Length: 120
Score: 103.40   Matches: 23

Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-070A-67 (1-120)

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Qy   3 GGCGAGTCA------------------------GGGTATTAGC------ 21
         ||||||||                        ||||||
Db  15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy  22 ------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                |||:::
Db  34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy  48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
         |||||||||||      |||||||||||||
Db  54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
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RESULT 14
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10021
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,153
;   FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769B
;   FILING DATE: 18-FEB-1998
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9000
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40

Alignment Scores:
Pred. No.:   0.00029   Length: 120
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1

Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-153-40 (1-120)

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Qy   3 GGCGAGTCA------------------------GGGTATTAGC------ 21
         ||||||||                        ||||||
Db  15 GlyGluSerLeuIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy  22 ------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                |||:::
Db  34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy  48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
         |||||||||||      |||||||||||||
Db  54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
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RESULT 15
US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10021
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,153
;   FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769B
;   FILING DATE: 18-FEB-1998
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9000
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

Alignment Scores:
Pred. No.:   0.00029   Length: 120
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26

DB: 4   Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-153-67 (1-120)

Qy   3 GGGCGAGTCA--------------------GGGTATTAGC------------ 21
        ||||||||| |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 --------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                   |||::: |||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCACATACAGCCCGTCCTTCCAAGGC 84
        ||||||||||||| |||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

Search completed: August 4, 2005, 19:04:16
Job time : 24.25 secs

OM nucleic - protein search, using frame_plus_n2p model

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GenCore version 5.1.6
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Run on:        August  4, 2005, 19:01:38 ; Search time 78.75 Seconds
                                           (without alignments)
                                           832.849 Million cell updates/sec

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Perfect score: 148
Sequence:      1 CGGGCGAGTCAGGGTATTAG........ACAGCCCGTCCTTCCAAGGC 84

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Searched:      1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters:      3505720

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123947_22665/app_query.fasta_1.5
-DB=Published_Applications_AA -QPMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPEXT=0.1 -YGAPOP=10 -DELOP=6 -DELEXT=0.1

Database :     Published_Applications_AA:*
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     5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
     6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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    11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
    12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
    13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
    14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
    15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
    16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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    18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
    19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
    20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
    21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
    22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	115	77.7	123	16	US-10-466-242-49	Sequence 49, Appl
2	113.3	76.6	411	16	US-10-769-144-12	Sequence 12, Appl
3	104.4	70.5	474	15	US-10-291-265-284	Sequence 284, App
4	104.2	70.4	301	14	US-10-002-631C-114	Sequence 114, App
5	103.4	69.9	98	9	US-09-850-165-89	Sequence 89, Appl
6	103.4	69.9	98	14	US-10-194-975-45	Sequence 45, Appl
7	103.4	69.9	98	14	US-10-125-687-16	Sequence 16, Appl
8	103.4	69.9	98	14	US-10-041-860-6	Sequence 6, Appli
9	103.4	69.9	98	14	US-10-041-860-301	Sequence 301, App
10	103.4	69.9	98	14	US-10-041-860-302	Sequence 302, App
11	103.4	69.9	98	14	US-10-041-860-312	Sequence 312, App
12	103.4	69.9	98	14	US-10-041-860-318	Sequence 318, App
13	103.4	69.9	98	14	US-10-041-860-320	Sequence 320, App
14	103.4	69.9	98	14	US-10-041-860-336	Sequence 336, App
15	103.4	69.9	98	14	US-10-041-860-367	Sequence 367, App
16	103.4	69.9	98	15	US-10-308-817-88	Sequence 88, Appl
17	103.4	69.9	98	15	US-10-032-037B-106	Sequence 106, App
18	103.4	69.9	98	15	US-10-032-037B-107	Sequence 107, App
19	103.4	69.9	98	15	US-10-032-037B-108	Sequence 108, App
20	103.4	69.9	98	15	US-10-029-988B-106	Sequence 106, App
21	103.4	69.9	98	15	US-10-029-988B-107	Sequence 107, App
22	103.4	69.9	98	15	US-10-029-988B-108	Sequence 108, App
23	103.4	69.9	98	15	US-10-032-423A-106	Sequence 106, App
24	103.4	69.9	98	15	US-10-032-423A-107	Sequence 107, App
25	103.4	69.9	98	15	US-10-032-423A-108	Sequence 108, App
26	103.4	69.9	98	15	US-10-453-698-88	Sequence 88, Appli
27	103.4	69.9	98	15	US-10-029-926B-106	Sequence 106, App
28	103.4	69.9	98	15	US-10-029-926B-107	Sequence 107, App
29	103.4	69.9	98	15	US-10-029-926B-108	Sequence 108, App
30	103.4	69.9	98	16	US-10-379-392-53	Sequence 53, Appl
31	103.4	69.9	98	16	US-10-769-144-30	Sequence 30, Appl
32	103.4	69.9	98	18	US-10-996-191-16	Sequence 16, App
33	103.4	69.9	109	16	US-10-800-197-144	Sequence 144, App
34	103.4	69.9	109	16	US-10-800-197-145	Sequence 145, App
35	103.4	69.9	109	16	US-10-800-197-146	Sequence 146, App
36	103.4	69.9	109	17	US-10-727-155-283	Sequence 283, App
37	103.4	69.9	109	17	US-10-727-155-291	Sequence 291, App
38	103.4	69.9	110	17	US-10-726-332-217	Sequence 217, App
39	103.4	69.9	116	17	US-10-727-155-100	Sequence 100, App
40	103.4	69.9	117	17	US-10-684-957-10	Sequence 10, Appl
41	103.4	69.9	117	17	US-10-684-957-30	Sequence 30, Appl
42	103.4	69.9	117	17	US-10-726-332-9	Sequence 9, Appli
43	103.4	69.9	117	17	US-10-726-332-138	Sequence 138, App
44	103.4	69.9	117	17	US-10-726-332-144	Sequence 144, App
45	103.4	69.9	118	17	US-10-726-332-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-10-466-242-49
; Sequence 49, Application US/10466242
; Sequence 49, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
;   APPLICANT: Drakenberg, Katarina
;   APPLICANT: Persson, Mats
;   TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
;   FILE REFERENCE: 0380-P03248US00
;   CURRENT APPLICATION NUMBER: US/10/466,242
;   CURRENT FILING DATE: 2004-01-16
;   PRIOR APPLICATION NUMBER: PCT/SE02/00044
;   PRIOR FILING DATE: 2002-01-14
;   NUMBER OF SEQ ID NOS: 56
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
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;  FEATURE:
;  NAME/KEY: PEPTIDE
;  LOCATION: (1)..(123)
;  OTHER INFORMATION: Clone 2b:7 VH
US-10-466-242-49

Alignment Scores:
Pred. No.:              0.000145        Length:              123
Score:                  115.00          Matches:             23
Percent Similarity:     55.32%          Conservative:        3
Best Local Similarity:  48.94%          Mismatches:          1
Query Match:            77.70%          Indels:              20
DB:                                     Gaps:                1

NOLAN463-2B.SEQ (1-84) x US-10-466-242-49 (1-123)

Qy      1 CGGGCGAGT----------------------------------------------------- 9
            |||||||||
Db     25 ArgAlaSerGlyTyrSerPheSerLeuPheTrpValAlaTrpValArgGlnMetProGly 44

Qy     10 CAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCACATACAGC 69
            |||:::..      |||::|| |||||||||||||||||||||||||||||||||
Db     45 GlnGlyLeu--GluTrpMetAlaIleIleTyrProGlyAspSerAspThrThrTyrSer 63

Qy     70 CCGTCCTTCCAAGGC 84
            |||||||||||:|||
Db     64 ProSerPheGluGly 68

RESULT 2
US-10-769-144-12
;  Sequence 12, Application US/10769144
;  Publication No. US2004024821SA1
;  GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT: Endres, Michael
;  APPLICANT: He, Lizhen
;  APPLICANT: Ramakrishna, Venky
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION: THEREFOR
;  FILE REFERENCE: MXI-301
;  CURRENT APPLICATION NUMBER: US/10/769,144
;  CURRENT FILING DATE: 2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 12
;  LENGTH: 411
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-769-144-12

Alignment Scores:
Pred. No.:              0.000293        Length:              411
Score:                  113.30          Matches:             26
Percent Similarity:     15.76%          Conservative:        0
Best Local Similarity:  15.76%          Mismatches:          2
Query Match:            76.55%          Indels:              137
DB:                                     Gaps:                1

NOLAN463-2B.SEQ (1-84) x US-10-769-144-12 (1-411)

Qy      1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCC---------------------------- 33
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Db     43 ArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGlnLysProGluLysAla 62

Qy     33 ------------------------------------------------------------ 33

Db     63 ProLysSerLeuIleTyrAlaAlaSerSerLeuSerGlnSerGlyValProSerArgPheSer 82

Qy     33 ------------------------------------------------------------ 33

Db     83 GlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 102
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Qy     33 ------------------------------------------------------------ 33

Db    103 AlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProArgThrPheGlyGlnGlyThrLys 122

Qy     33 ------------------------------------------------------------ 33

Db    123 ValGluIleLysGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlu 142

Qy     33 ------------------------------------------------------------ 33

Db    143 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuArgIleSer 162

Qy     33 ------------------------------------------------------------ 33

Db    163 CysLysGlyGlyAspSerPheThrThrTyrGlyIleTrpValArgGlnMetPro 182

Qy     34 ------------------------ATCATCTATCCTGGTGACTCTGATACCACATACAGC 69
                                  |||||||||||||||||||||||||||||||||
Db    183 GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrIleTyrSer 202

Qy     70 CCGTCCTTCCAAGGC 84
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Db    203 ProSerPheGlnGly 207

RESULT 3
US-10-291-265-284
;  Sequence 284, Application US/10291265
;  Publication No. US20030232054A1
;  GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT: Tang et al
;  TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-017 (785)
;  CURRENT APPLICATION NUMBER: US/10/291,265
;  CURRENT FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 284
;  LENGTH: 474
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-291-265-284

Alignment Scores:
Pred. No.:              0.00333         Length:              474
Score:                  104.40          Matches:             23
Percent Similarity:     47.17%          Conservative:        2
Best Local Similarity:  43.40%          Mismatches:          2
Query Match:            70.54%          Indels:              26
DB:                                     Gaps:                2

NOLAN463-2B.SEQ (1-84) x US-10-291-265-284 (1-474)

Qy      3 GGGCGAGTCA----------------------------------GGGTATTAGC------- 21
            ||||||||||                                  |||||||||
Db     34 GlyGluSerValLysIleSerCysLysGlySerGlyTyr-SerPheSerAspTyrTrpVa 53

Qy     22 --------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                            :::|||||||||||||||||||||||
Db     53 lAlaTrpValArgGlnSerProAspLysGlyLeuAlaTrpGlyIleIleTyrMetGlyIleIleTyrProGl 73

Qy     48 TGACTTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
            ||||||||||||||||||||||||||||||||||
Db     73 yAspSerAspThrArgTyrSerProSerPheGlnGly 85
```

RESULT 4
US-10-002-631C-114
; Sequence 114, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (2)...(66)
; OTHER INFORMATION: Xaa = any amino acid
US-10-002-631C-114

Alignment Scores:
Pred. No.:   0.0032
Score: 104.20
Percent Similarity: 66.67%
Best Local Similarity: 57.58%
Query Match: 70.41%
DB: 14

Length: 301
Matches: 19
Conservative: 3
Mismatches: 3
Indels: 8
Gaps: 0

NOLAN463-2B.SEQ (1-84) x US-10-002-631C-114 (1-301)

Qy   2 GGGCGAGTCAGGTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCA 61
        ||||:: |||:: |||||||||||||||||||||||||||||||||||
Db   92 GlyLys-----GlyLeu---GluTrpMetGlyIleIleIleTyrProGlyAspSerAspAlaT 109

Qy   62 CATACAGCCCGTCCTTCCAAGGC 84
        ||||||||||||||||||||||
Db 109 hrTyrSerProSerPheGlnGly 116

RESULT 5
US-09-850-165-89
; Sequence 89, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 98
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (19)
; OTHER INFORMATION: Arg or Lys
US-09-850-165-89

Alignment Scores:
Pred. No.:   0.00316
Score: 103.40
Percent Similarity: 45.28%
Best Local Similarity: 43.40%
Query Match: 69.86%
DB: 9

Length: 98
Matches: 23
Conservative: 1
Mismatches: 3
Indels: 26
Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-850-165-89 (1-98)

Qy   3 GGGGAGTCA-----------------------GGGTATTAGC--------- 21
        |||||||||| |||||| |||
Db   15 GlyGluSerLeu***IleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 -----------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                           ||:||||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
        |||||||||| |||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 6
US-10-194-975-45
; Sequence 45, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-45

Alignment Scores:
Pred. No.:   0.00316
Score: 103.40
Percent Similarity: 45.28%
Best Local Similarity: 43.40%
Query Match: 69.86%
DB: 14

Length: 98
Matches: 23
Conservative: 1
Mismatches: 3
Indels: 26
Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-194-975-45 (1-98)

Qy   3 GGGGAGTCA-----------------------GGGTATTAGC--------- 21
        |||||||||| |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 -----------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                           ||:||||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
        |||||||||| |||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 7
US-10-125-687-16

```
Qy    3 GGGGAGTCA-----------------------GGGTATTAGC-      21
        ||||||||                        ||||| ||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 -------------------AGCTGGTTAGCCATCATCATCCTGG  47
                           ||:::||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
        |||||||||||   |||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 9
US-10-041-860-301
; Sequence 301, Application US/10041860
; Publication No. US2003015709A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-301

Alignment Scores:
Pred. No.:   0.00316   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 14   Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-301 (1-98)

```
Qy    3 GGGGAGTCA-----------------------GGGTATTAGC-      21
        ||||||||                        ||||| ||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 -------------------AGCTGGTTAGCCATCATCATCCTGG  47
                           ||:::||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
        |||||||||||   |||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 10
US-10-041-860-302
; Sequence 302, Application US/10041860
; Publication No. US2003015709A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard

; Sequence 16, Application US/10125687
; Publication No. US2003054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 16
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-687-16

Alignment Scores:
Pred. No.:   0.00316   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 14   Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-125-687-16 (1-98)

```
Qy    3 GGGGAGTCA-----------------------GGGTATTAGC-      21
        ||||||||                        ||||| ||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 -------------------AGCTGGTTAGCCATCATCATCCTGG  47
                           ||:::||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
        |||||||||||   |||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

RESULT 8
US-10-041-860-6
; Sequence 6, Application US/10041860
; Publication No. US2003015709A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-6

Alignment Scores:
Pred. No.:   0.00316   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 14   Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-6 (1-98)
```

; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 23
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 23
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-302

Alignment Scores:
Pred. No.:                0.00316          Length:         98
Score:                    103.40           Matches:        23
Percent Similarity:       45.28%           Conservative:   1
Best Local Similarity:    43.40%           Mismatches:     3
Query Match:              69.86%           Indels:         26
DB:                       14               Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-302 (1-98)

Qy    3 GGCGAGTCA------------------------GGGTATTAGC----------- 21
         ||||||||                         |||||| |||
Db   15 GlyGluSerLeuLysIleSerCys***GlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                 |||:::  ||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         ||||||||||     |||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 11
US-10-041-860-312
; Sequence 312, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-312

Alignment Scores:
Pred. No.:                0.00316          Length:         98
Score:                    103.40           Matches:        23
Percent Similarity:       45.28%           Conservative:   1
Best Local Similarity:    43.40%           Mismatches:     3
Query Match:              69.86%           Indels:         26
DB:                       14               Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-312 (1-98)

Qy    3 GGCGAGTCA------------------------GGGTATTAGC----------- 21
         ||||||||                         |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                 |||:::  ||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         ||||||||||     |||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 12
US-10-041-860-318
; Sequence 318, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-318

Alignment Scores:
Pred. No.:                0.00316          Length:         98
Score:                    103.40           Matches:        23
Percent Similarity:       45.28%           Conservative:   1
Best Local Similarity:    43.40%           Mismatches:     3
Query Match:              69.86%           Indels:         26
DB:                       14               Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-318 (1-98)

Qy    3 GGCGAGTCA------------------------GGGTATTAGC----------- 21
         ||||||||                         |||||| |||
Db   15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------------AGCTGGTTAGCCATCATCATCCTGG 47
                                 |||:::  ||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
         ||||||||||     |||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 13
US-10-041-860-320
; Sequence 320, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.

Alignment Scores:
Pred. No.:                0.00316          Length:         98
Score:                    103.40           Matches:        23

```
;   APPLICANT:  Jia, Xiao-Chi
;   APPLICANT:  Feng, Xiao
;   APPLICANT:  Yang, Xiao-Dong
;   APPLICANT:  Chen, Francine
;   APPLICANT:  Gazit, Gadi
;   APPLICANT:  Weber, Richard
;   APPLICANT:  Bezabeh, Binyam
;   TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: ABGENIX.051A
;   CURRENT APPLICATION NUMBER: US/10/041,860
;   CURRENT FILING DATE:  2002-01-07
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   NUMBER OF SEQ ID NOS: 377
;   SEQ ID NO 320
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 68
;   OTHER INFORMATION: Xaa = Any Amino Acid
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 68
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-320

Alignment Scores:
Pred. No.:                         0.00316        Length:         98
Score:                             103.40         Matches:        23
Percent Similarity:                45.28%         Conservative:   1
Best Local Similarity:             43.40%         Mismatches:     3
Query Match:                       69.86%         Indels:         26
DB:                                14             Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-320 (1-98)

Qy     3 GGCGAGTCA-----------------------GGGTATTAGC------------ 21
           ||||||||                        ||||| ||
Db    15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy    22 -----------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                 |||:::|||||||||||||||
Db    34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy    48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
           ||||||||||||||||||||||||
Db    54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 14
US-10-041-860-336
;   Sequence 336, Application US20030157109A1
;   Publication No. US20030157109A1
;   GENERAL INFORMATION:
;   APPLICANT:  Corvalan, Jose R.F.
;   APPLICANT:  Jia, Xiao-Chi
;   APPLICANT:  Feng, Xiao
;   APPLICANT:  Yang, Xiao-Dong
;   APPLICANT:  Chen, Francine
;   APPLICANT:  Gazit, Gadi
;   APPLICANT:  Weber, Richard
;   APPLICANT:  Bezabeh, Binyam
;   TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: ABGENIX.051A
;   CURRENT APPLICATION NUMBER: US/10/041,860
;   CURRENT FILING DATE:  2002-01-07
;   NUMBER OF SEQ ID NOS: 377
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 336
;   LENGTH: 98
;   TYPE: PRT
```

```
;   ORGANISM: homo sapiens
US-10-041-860-336

Alignment Scores:
Pred. No.:                         0.00316        Length:         98
Score:                             103.40         Matches:        23
Percent Similarity:                45.28%         Conservative:   1
Best Local Similarity:             43.40%         Mismatches:     3
Query Match:                       69.86%         Indels:         26
DB:                                14             Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-336 (1-98)

Qy     3 GGCGAGTCA-----------------------GGGTATTAGC------------ 21
           ||||||||                        ||||| ||
Db    15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy    22 -----------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                 |||:::|||||||||||||||
Db    34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy    48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
           ||||||||||||||||||||||||
Db    54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 15
US-10-041-860-367
;   Sequence 367, Application US20030157109A1
;   Publication No. US20030157109A1
;   GENERAL INFORMATION:
;   APPLICANT:  Corvalan, Jose R.F.
;   APPLICANT:  Jia, Xiao-Chi
;   APPLICANT:  Feng, Xiao
;   APPLICANT:  Yang, Xiao-Dong
;   APPLICANT:  Chen, Francine
;   APPLICANT:  Gazit, Gadi
;   APPLICANT:  Weber, Richard
;   APPLICANT:  Bezabeh, Binyam
;   TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: ABGENIX.051A
;   CURRENT APPLICATION NUMBER: US/10/041,860
;   CURRENT FILING DATE:  2002-01-07
;   NUMBER OF SEQ ID NOS: 377
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 367
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-367

Alignment Scores:
Pred. No.:                         0.00316        Length:         98
Score:                             103.40         Matches:        23
Percent Similarity:                45.28%         Conservative:   1
Best Local Similarity:             43.40%         Mismatches:     3
Query Match:                       69.86%         Indels:         26
DB:                                14             Gaps:           2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-367 (1-98)

Qy     3 GGCGAGTCA-----------------------GGGTATTAGC------------ 21
           ||||||||                        ||||| ||
Db    15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy    22 -----------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                 |||:::|||||||||||||||
Db    34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

Qy    48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
           ||||||||||||||||||||||||
Db    54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

nolan463-2b.seq.rapb

Fri Aug 5 09:28:06 2005

Search completed: August 4, 2005, 19:30:18
Job time : 79.75 secs

```
          GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on:   August  4, 2005, 18:42:17 ; Search time 17.75 Seconds
                                      (without alignments)
                                      910.671 Million cell updates/sec

Title:            NOLAN463-2B.SEQ
Perfect score:    148
Sequence:         1 CGGGCGAGTCAGGGTATTAG........ACAGCCCGTCCTTCCAAGGC 84

Scoring table:    BLOSUM62
                  Xgapop  10.0 , Xgapext  0.1
                  Ygapop  10.0 , Ygapext  0.1
                  Fgapop   6.0 , Fgapext  0.1
                  Delop    6.0 , Delext   0.1

Searched:         283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:   566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123944_22592/app_query.fasta_1.5
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN_1_1_77 @runat_04082005_123944_22592 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :     PIR_79:*
          1: pir1:*
          2: pir2:*
          3: pir3:*
          4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
              %
Result      Query
No.  Score  Match Length DB  ID       Description
---- -----  ----- ------ --  --       -----------
  1  108.7  73.4   102   2  PH1277    Ig heavy chain V r
  2  106.7  72.1   127   2  PH1409    Ig heavy chain V r
  3  103.4  69.9    98   2  PH1274    Ig heavy chain V r
  4  103.4  69.9    98   2  S26907    Ig heavy chain V r
  5  103.4  69.9   101   2  S12428    Ig heavy chain V r
  6  103.4  69.9   101   2  S12424    Ig heavy chain V r
  7  103.4  69.9   102   2  PH1266    Ig heavy chain V r
  8  103.4  69.9   102   2  PH1279    Ig heavy chain V r
  9  103.4  69.9   102   2  PH1281    Ig heavy chain V r
 10  103.4  69.9   102   2  PH1244    Ig heavy chain V r
 11  103.4  69.9   102   2  PH1272    Ig heavy chain V r
 12  103.4  69.9   102   2  PH1282    Ig heavy chain V r
 13  103.4  69.9   102   2  PH1258    Ig heavy chain V r
 14  103.4  69.9   102   2  PH1264    Ig heavy chain V r
```

```
 15  103.4  69.9   102   2  PH1259    Ig heavy chain V r
 16  103.4  69.9   102   2  PH1273    Ig heavy chain V r
 17  103.4  69.9   102   2  PH1249    Ig heavy chain V r
 18  103.4  69.9   102   2  PH1271    Ig heavy chain V r
 19  103.4  69.9   102   2  PH1278    Ig heavy chain V r
 20  103.4  69.9   113   2  PH1428    Ig heavy chain V r
 21  103.4  69.9   115   2  PH1557    Ig heavy chain V r
 22  103.4  69.9   117   2  A28846    Ig heavy chain pre
 23  103.4  69.9   123   2  PH1423    Ig heavy chain V r
 24  103.4  69.9   123   2  S38492    Ig heavy chain - h
 25  103.4  69.9   123   2  C36006    Ig heavy chain V r
 26  103.4  69.9   127   2  PH1414    Ig heavy chain V r
 27  103.4  69.9   127   2  PH1411    Ig heavy chain V r
 28  103.4  69.9   128   2  S16685    Ig heavy chain V r
 29  103.4  69.9   134   2  PH1422    Ig heavy chain V r
 30  103.4  69.9   136   2  A49047    Ig heavy chain V r
 31  103.4  69.9   139   2  PH1558    Ig heavy chain V r
 32  103.2  69.7   102   2  PH1267    Ig heavy chain V r
 33  103.2  69.7   102   2  PH1280    Ig heavy chain V r
 34  103.2  69.7   104   2  B36006    Ig heavy chain V r
 35  103.2  69.7   117   2  S19670    Ig heavy chain V r
 36  103.2  69.7   136   2  PH1559    Ig heavy chain V r
 37  102.4  69.2    98   2  PH0877    Ig heavy chain V r
 38  101    68.2   102   2  PH1248    Ig heavy chain V r
 39  100.4  67.8   102   2  PH1252    Ig heavy chain V r
 40   99.4  67.2   123   2  PH1413    Ig heavy chain V r
 41   98.4  66.5   102   2  PH1265    Ig heavy chain V r
 42   98.3  66.4   126   2  PH1416    Ig heavy chain V r
 43   98.3  66.4   126   2  PH1419    Ig heavy chain V r
 44   98.2  66.4    86   2  S12580    Ig heavy chain V r
 45   97.4  65.8   102   2  PH1247    Ig heavy chain V r
```

```
                         ALIGNMENTS

RESULT 1
PH1277
Ig heavy chain V region (clone PBL8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1277
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:                    3.06e-05      Length:            102
Score:                        108.70        Matches:            19
Percent Similarity:           76.67%        Conservative:        4
Best Local Similarity:        63.33%        Mismatches:          4
Query Match:                  73.45%        Indels:              3
DB:                           2             Gaps:                0

NOLAN463-2B.SEQ (1-84) x PH1277 (1-102)

Qy     1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGTGACTCTGATACC  60
            ::::|||  :::||:|:::    |||:::  |||::::|  |||||||||||||||||
Db    44 LysAlaGlyLysGlyLeu---GluTrpMetGlyIleIleTyrProGlyAspSerAspThr  62

Qy    61 ACATACAGCCCGTCCTTCCAAGGC  84
         |||||||||||||||||||||||
Db    63 ArgTyrSerProSerPheGlnGly  70

RESULT 2
PH1409
```

Ig heavy chain V region (clone P1-51) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 17-Mar-1999
C;Accession: PH1409
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1409
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   5.59e-05   Length: 127
Score: 106.70   Matches: 19
Percent Similarity: 73.33%   Conservative: 3
Best Local Similarity: 63.33%   Mismatches: 5
Query Match: 72.09%   Indels: 3
DB: 2   Gaps: 0

NOLAN463-2B.SEQ (1-84) x PH1409 (1-127)

Qy   1 CGGGCGGAGTCAGGGTATTAGCAGCGGTTAGCCATCATCCTGGTGACTTCTGATACC 60
            ||| :::|||||:: |||||::: |||||||||||||||||||||||||||
Db   40 ArgProGlyLysGlyLeu--GluTrpMetGlyIleIleIlePheTyrProGlyAspSerAspThr 58

Qy   61 ACATACAGCCCGTCCTTCCAAGGC 84
            |||||||||||||||||||||||
Db   59 ArgTyrSerProSerPheGlnGly 66

RESULT 3
PH1274
Ig heavy chain V region (clone PBL5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1274
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1274
A;Molecule type: DNA
A;Residues: 1-98 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.:   0.000145   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 2   Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1274 (1-98)

Qy   3 GGGAGTCA----------GGGTATTAGC---------- 21
            |||||||| |||| |||
Db   19 GlyGluSerLeuLysLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 38

Qy   22 ------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                              |||:|| |||||||||||||||||
Db   38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 58

Qy   48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
            ||||||||||| |||||||||||||||||||||||
Db   58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70

RESULT 4
S26907
Ig heavy chain V region (DP-73) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26907
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v.
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26907
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12373; NID:g32965; PIDN:CAA78243.1; PID:g32966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000145   Length: 98
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 2   Gaps: 2

NOLAN463-2B.SEQ (1-84) x S26907 (1-98)

Qy   3 GGGAGTCA----------GGGTATTAGC---------- 21
            |||||||| |||| |||
Db   15 GlyGluSerLeuLysLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

Qy   22 ------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                              |||:|| |||||||||||||||||
Db   34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54

Qy   48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
            ||||||||||| |||||||||||||||||||||||
Db   54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 5
S12428
Ig heavy chain V region (5JB) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S12428
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12428
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Cross-references: EMBL:X56367
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000145   Length: 101
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 26
Query Match: 69.86%   Indels: 26
DB: 2   Gaps: 2

NOLAN463-2B.SEQ (1-84) x S12428 (1-101)

Qy   3 GGGAGTCA----------GGGTATTAGC---------- 21
            |||||||| |||||| |||

```
Db  18 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 37
Qy  22 ----------------------------------------AGCTGGTTAGCCATCATCCTGG 47
           ||:::  |||||||||||||
Db  37 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 57
```

RESULT 6
S12424
Ig heavy chain V region (5) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C;Accession: S12424; S12425; S12426; S12427; S12429; S12432
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12424
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Cross-references: EMBL:X56372
A;Molecule type: DNA
A;Residues: 1-101 <SA3>
A;Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT
A;Accession: S12425
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA2>
A;Cross-references: EMBL:X56373
A;Accession: S12426
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA3>
A;Cross-references: EMBL:X56370
A;Accession: S12427
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA4>
A;Cross-references: EMBL:X56368
A;Accession: S12429
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA5>
A;Cross-references: EMBL:X56369
A;Accession: S12432
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA6>
A;Cross-references: EMBL:X56371
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000145   Length: 101
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 2   Gaps: 2

NOLAN463-2B.SEQ (1-84) x S12424 (1-101)

```
Qy   3 GGCGAGTCA------------------------------------GGGTATTAGC------ 21
        |||||||||                                    ||| |||
Db  18 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 37
Qy  22 ----------------------------------------AGCTGGTTAGCCATCATCCTGG 47
           ||:::  |||||||||||||
Db  37 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 57
```

```
Qy  48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
        |||||||||||||||||||||||||
Db  57 yAspSerAspThrArgTyrSerProSerPheGlnGly 69
```

RESULT 7
PH1266
Ig heavy chain V region (clone VERG5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1266
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1266
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000145   Length: 102
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 1
Query Match: 69.86%   Indels: 26
DB: 2   Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1266 (1-102)

```
Qy   3 GGCGAGTCA------------------------------------GGGTATTAGC------ 21
        |||||||||                                    ||| |||
Db  19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 38
Qy  22 ----------------------------------------AGCTGGTTAGCCATCATCCTGG 47
           ||:::  |||||||||||||
Db  38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58
```

```
Qy  48 TGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 84
        |||||||||||||||||||||||||
Db  58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70
```

RESULT 8
PH1279
Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1279
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1279
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000145   Length: 102
Score: 103.40   Matches: 23
Percent Similarity: 45.28%   Conservative: 1
Best Local Similarity: 43.40%   Mismatches: 3
Query Match: 69.86%   Indels: 26
DB: 2   Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1279 (1-102)

```
Qy   3 GGCGAGTCA------------------------------------GGGTATTAGC------ 21
```

Left column:

```
Db        |||||||||
       19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 38
                                                 |||||| |||
Qy     22 --------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                                 ||||||||||||
Db     38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58

Qy     48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          ||||||||||||| |||||||||||||||||
Db     58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70

RESULT 9
PH1281
Ig heavy chain V region (clone PBL12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1281
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1281
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:                   0.000145        Length:             102
Score:                       103.40          Matches:            23
Percent Similarity:          45.28%          Conservative:       1
Best Local Similarity:       43.40%          Mismatches:         3
Query Match:                 69.86%          Indels:             26
DB:                                          Gaps:               2

NOLAN463-2B.SEQ (1-84) x PH1244 (1-102)

Qy      3 GGCGAGTCA---------------------------------GGGTATTAGC- 21
          |||||||||                                 |||||| |||
Db     19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 38

Qy     22 --------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                                 ||||:::||||||||||
Db     38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58

Qy     48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          ||||||||||||| |||||||||||||||||
Db     58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70

RESULT 10
PH1244
Ig heavy chain V region (clone CORD2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1244
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1244
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:                   0.000145        Length:             102
Score:                       103.40          Matches:            23
Percent Similarity:          45.28%          Conservative:       1
```

Right column:

```
Best Local Similarity:       43.40%          Mismatches:         3
Query Match:                 69.86%          Indels:             26
DB:                                          Gaps:               2

NOLAN463-2B.SEQ (1-84) x PH1244 (1-102)

Qy      3 GGGAGTCA---------------------------------GGGTATTAGC- 21
          |||||||||                                 |||||| |||
Db     19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 38

Qy     22 --------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                                 ||||:::||||||||||
Db     38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58

Qy     48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          ||||||||||||| |||||||||||||||||
Db     58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70

RESULT 11
PH1272
Ig heavy chain V region (clone PBL3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1272
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1272
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:                   0.000145        Length:             102
Score:                       103.40          Matches:            23
Percent Similarity:          45.28%          Conservative:       1
Best Local Similarity:       43.40%          Mismatches:         3
Query Match:                 69.86%          Indels:             26
DB:                                          Gaps:               2

NOLAN463-2B.SEQ (1-84) x PH1272 (1-102)

Qy      3 GGCGAGTCA---------------------------------GGGTATTAGC- 21
          |||||||||                                 |||||| |||
Db     19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 38

Qy     22 --------------------------------------AGCTGGTTAGCCATCATCTATCCTGG 47
                                                 ||||:::||||||||||
Db     38 eAlaTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58

Qy     48 TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC 84
          ||||||||||||| |||||||||||||||||
Db     58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70

RESULT 12
PH1282
Ig heavy chain V region (clone PBL13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
```

C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                  0.000145      Length:         102
Percent Similarity:     103.40%       Matches:        23
Best Local Similarity:  45.28%        Conservative:   1
Query Match:            43.40%        Mismatches:     3
DB:                     69.86%        Indels:         26
                        2             Gaps:           2
```

```
NOLAN463-2B.SEQ (1-84) x PH1282 (1-102)

Qy    3  GGCGAGTCA--------------GGGTATTAGC------------  21
         |||||||||              |||||| |||
Db   19  GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl  38

Qy   22  --------------------------AGCTGGTTAGCCATCATCTATCCTGG  47
                                   |||:::  |||||||||||||
Db   38  eGlyTrpValArgGlnThrProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl  58

Qy   48  TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC  84
         ||||||||||||||||||||||||||||||||||||||
Db   58  yAspSerAspThrArgTyrSerProSerPheGlnGly  70
```

RESULT 13
PH1258
Ig heavy chain V region (clone CD-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1258
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1258
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                  0.000145      Length:         102
Percent Similarity:     103.40%       Matches:        23
Best Local Similarity:  45.28%        Conservative:   1
Query Match:            43.40%        Mismatches:     3
DB:                     69.86%        Indels:         26
                        2             Gaps:           2
```

```
NOLAN463-2B.SEQ (1-84) x PH1258 (1-102)

Qy    3  GGCGAGTCA--------------GGGTATTAGC------------  21
         |||||||||              |||||| |||
Db   19  GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheIleAsnTyrTrpIl  38

Qy   22  --------------------------AGCTGGTTAGCCATCATCTATCCTGG  47
                                   |||:::  |||||||||||||
Db   38  eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl  58

Qy   48  TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC  84
         ||||||||||||||||||||||||||||||||||||||
Db   58  yAspSerAspThrArgTyrSerProSerPheGlnGly  70
```

RESULT 14
PH1264
Ig heavy chain V region (clone VERG3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1264
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992

A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell [from adult PBL]
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1264
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                  0.000145      Length:         102
Percent Similarity:     103.40%       Matches:        23
Best Local Similarity:  45.28%        Conservative:   1
Query Match:            43.40%        Mismatches:     3
DB:                     69.86%        Indels:         26
                        2             Gaps:           2
```

```
NOLAN463-2B.SEQ (1-84) x PH1264 (1-102)

Qy    3  GGCGAGTCA--------------GGGTATTAGC------------  21
         |||||||||              |||||| |||
Db   19  GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheSerSerTyrTrpIl  38

Qy   22  --------------------------AGCTGGTTAGCCATCATCTATCCTGG  47
                                   |||:::  |||||||||||||
Db   38  eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl  58

Qy   48  TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC  84
         ||||||||||||||||||||||||||||||||||||||
Db   58  yAspSerAspThrArgTyrSerProSerPheGlnGly  70
```

RESULT 15
PH1259
Ig heavy chain V region (clone CD-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1259
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1259
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                  0.000145      Length:         102
Percent Similarity:     103.40%       Matches:        23
Best Local Similarity:  45.28%        Conservative:   1
Query Match:            43.40%        Mismatches:     3
DB:                     69.86%        Indels:         26
                        2             Gaps:           2
```

```
NOLAN463-2B.SEQ (1-84) x PH1259 (1-102)

Qy    3  GGCGAGTCA--------------GGGTATTAGC------------  21
         |||||||||              |||||| |||
Db   19  GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl  38

Qy   22  --------------------------AGCTGGTTAGCCATCATCTATCCTGG  47
                                   |||:::  |||||||||||||
Db   38  eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl  58

Qy   48  TGACTCTGATACCACCATACAGCCCGTCCTTCCAAGGC  84
         ||||||||||||||||||||||||||||||||||||||
Db   58  yAspSerAspThrArgTyrSerProSerPheGlnGly  70
```

nolan463-2b.seq.rpr

Fri Aug 5 09:28:07 2005

Search completed: August 4, 2005, 19:02:37
Job time : 18.75 secs

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     August   4, 2005, 18:23:15 ; Search time 80.75 Seconds
                                         (without alignments)
                                         1065.378 Million cell updates/sec

Title:          NOLAN463-2B.SEQ
Perfect score:  148
Sequence:       1 CGGGCGAGTCAGGGTATTAG........ACAGCCCGTCCTTCCAAGGC 84

Scoring table:  BLOSUM62
                Xgapop  10.0 , Xgapext  0.1
                Ygapop  10.0 , Ygapext  0.1
                Fgapop   6.0 , Fgapext  0.1
                Delop    6.0 , Delext   0.1

Searched:       1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:        3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123944_22581/app_query.fasta_1.5
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN 1_1_305 @runat 04082005_123944_22581 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=120 -THREADS=0 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :       UniProt 03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84.7	57.2	118	2	Q9ZIC4	Q9zic4 mus musculu
2	77.7	52.5	474	2	Q8R3H6	Q8r3h6 mus musculu
3	76.7	51.8	111	2	Q9D9D8	Q9d9b8 mus musculu
4	75.7	51.1	614	2	Q7TWT6	Q7tmt6 mus musculu
5	74.7	50.5	117	2	HV06_MOUSE	P01750 mus musculu
6	74.7	50.5	117	2	HVS2_MOUSE	P06327 mus musculu
7	73.7	49.8	110	2	Q9JL83	Q9jl83 mus musculu
8	73.7	49.8	481	2	Q91WT1	Q91wt1 mus musculu
9	72.7	49.1	464	2	Q6PF95	Q6pf95 mus musculu
10	71.7	48.4	463	2	Q99LC4	Q99lc4 mus musculu
11	68.2	46.1	125	1	HV1F_HUMAN	P06326 homo sapien
12	67.7	45.7	117	1	HV05_MOUSE	P01749 mus musculu
13	66.7	45.1	143	2	Q91V67	Q91v67 mus musculu
14	65.5	44.3	236	2	Q6GMX8	Q6gmx8 homo sapien
15	64.7	43.7	136	2	Q7TPE3	Q7tpe3 mus musculu
16	63.8	43.1	370	2	Q7N4R1	Q7n4r1 photorhabdu
17		63.7	43.0	121	2	Q9UL96	Q9ul96 homo sapien
18		63.7	42.4	143	2	Q92Q0	Q92q0 mus musculu
19		62.7	42.2	147	2	Q92S3	Q92s3 mus musculu
20		62.5	42.2	1680	2	Q9P1Z9	Q9p1z9 homo sapien
21	c	62.3	39.0	295	2	Q8ZIR4	Q8z1r4 salmonella
22	c	62.3	39.0	295	2	Q8ZKG0	Q8zkg0 salmonella
23		62	41.9	98	2	Q6B6V3	Q6b6v3 oryctolagus
24		62	41.9	98	2	Q6B6W5	Q6b6w5 oryctolagus
25		62	41.9	99	2	Q6B6B4	Q6b6b4 oryctolagus
26		62	41.9	99	2	Q6B6S7	Q6b6s7 oryctolagus
27		61.7	41.7	117	1	HV1B_HUMAN	P01743 homo sapien
28		61.7	41.7	124	2	Q9UL92	Q9ul92 homo sapien
29	c	61.6	38.5	302	2	Q9I9C3	Q9i9c3 anguilla an
30		61.1	41.3	4335	2	Q6NA45	Q6na45 rhodopseudo
31		60.7	41.0	143	2	Q924P9	Q924p9 mus musculu
32		60.7	41.0	330	2	Q93KW0	Q93kw0 streptomyce
33		60.7	41.0	481	2	Q91WT3	Q91wt3 mus musculu
34		60.7	41.0	1189	2	Q8NSU0	Q8nsu0 corynebacte
35		60.7	41.0	1208	2	Q6M7I4	Q6m7i4 corynebacte
36		60.6	40.9	733	2	Q65BI3	Q65bi3 oryza sativ
37		60.5	40.9	117	1	KV1I_HUMAN	P01601 homo sapien
38		60.2	40.7	390	2	Q7S6A9	Q7s6a9 neurospora
39		60.1	40.6	763	2	Q7Q5F3	Q7q5f3 anopheles g
40		60	40.5	537	2	Q6GNX4	Q6gnx4 xenopus lae
41	c	59.8	37.4	524	2	Q6ZM46	Q6zm46 brachydanio
42		59.7	40.3	120	1	HV03_MOUSE	P01747 mus musculu
43		59.7	40.3	487	2	Q65ZL2	Q65zl2 mus sp. fv/
44		59.5	40.2	107	1	KV1D_HUMAN	P01596 homo sapien
45		59.5	40.2	117	1	KV1J_HUMAN	P01602 homo sapien

```
                              ALIGNMENTS

RESULT 1
Q9ZIC4
ID   Q9ZIC4        PRELIMINARY;       PRT;    118 AA.
AC   Q9ZIC4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Balb/c;
RX   MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P..
RA   Matis L.A., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Mol. Immunol. 34:441-452(1997).
DR   EMBL; U78801; AAD00293.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    118    118
SQ   SEQUENCE   118 AA;   13036 MW;  90EC559D31EC4FC CRC64;

Alignment Scores:
Pred. No.:                              0.141
Score:                                 84.70             Length:            118
Percent Similarity:                    63.33%            Matches:            14
Best Local Similarity:                 46.67%            Conservative:        5
Query Match:                           57.23%            Mismatches:          8
DB:                                         2            Indels:              3
                                                         Gaps:                0
```

```
NOLAN463-2B.SEQ (1-84) x Q921C4 (1-118)

Qy         1 CGGGCGAGTCAGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
             ||||||||:::      |||:::      ||||||
Db        40 ArgProGlyGlnGlyLeu--GluTrpIleGlyAlaIleTyrProGlyAspGlyAspThr 58

Qy        61 ACATACAGCCCGTCCTTCCAAGGC 84
             :::|||::::      ||:::|||
Db        59 SerTyrThrGlnLysPheArgGly 66

RESULT 2
Q8R3H6
ID   Q8R3H6;         PRELIMINARY;         PRT;         474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AU044919 protein.
GN   Name=AU044919;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
DR   HSSP; P01869; 1CL7.
DR   MGD; MGI:2144967; AU044919.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Alignment Scores:
Pred. No.:                   1,4         Length:          474
Score:                     77.70         Matches:          14
Percent Similarity:        60.00%        Conservative:      4
Best Local Similarity:     46.67%        Mismatches:        9
Query Match:               52.50%        Indels:            3
```

```
DB:                                         2         Gaps:         0

NOLAN463-2B.SEQ (1-84) x Q8R3H6 (1-474)

Qy         1 CGGGCGAGTCAGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
             |||      :::|||:::      |||:::      ||||||
Db        59 ArgProGlyLysGlyLeu--GluTrpIleGlyArgIlePheProGlyAspGlyAspThr 77

Qy        61 ACATACAGCCCGTCCTTCCAAGGC 84
             |||||||      ||||||
Db        78 HisTyrSerGlyLysPheGlnGly 85

RESULT 3
Q9D9B8
ID   Q9D9B8;         PRELIMINARY;         PRT;         111 AA.
AC   Q9D9B8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE   library, clone:1700110I11 product:immunoglobulin heavy chain 6 (heavy
DE   chain of IgM), full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=9927253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085560; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384 format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
```

RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato C.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shinagawa Y., Shirai T., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK007163; BAB24877.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   111 AA;   11976 MW;   874DF7BD98BD7B2 CRC64;

Alignment Scores:
Pred. No.:   1.49   Length: 111
Score: 76.70   Matches: 13
Percent Similarity: 60.00%   Conservative: 5
Best Local Similarity: 43.33%   Mismatches: 9
Query Match: 51.82%   Indels: 3
DB: Gaps: 0

NOLAN463-2B.SEQ (1-84) x Q9D9B8 (1-111)

Qy   1 CGGGCGAGTCAGGGTATTAGCAGTGGTTAGCCATCATCTATCCTGTGACTCTGATACC 60
           ||| :::|||::: :::||||||: |||||||||||||||| |||||
Db   46 ArgProGlyLysGlyLeu---GluTrpIleGlyArgIleTyrProGlyAspGlyAspThr 64

Qy   61 ACATACAGCCCGTCCTTCCAAGGC 84
           |||::: ||||||||:::|||
Db   65 AsnTyrAsnGlyLysPheLysGly 72

RESULT 4
Q7TMT6
ID   Q7TMT6   PRELIMINARY;   PRT;   614 AA.
AC   Q7TMT6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MGC60843 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human

---

RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053409; AAH53409.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3
SQ   SEQUENCE   614 AA;   67746 MW;   839BAF3B8D124F89 CRC64;

Alignment Scores:
Pred. No.:   2.64   Length: 614
Score: 75.70   Matches: 12
Percent Similarity: 60.00%   Conservative: 6
Best Local Similarity: 40.00%   Mismatches: 9
Query Match: 51.15%   Indels: 3
DB: Gaps: 0

NOLAN463-2B.SEQ (1-84) x Q7TMT6 (1-614)

Qy   1 CGGGCGAGTCAGGGTATTAGCAGTGGTTAGCCATCATCTATCCTGTGACTCTGATACC 60
           ||| :::|||::: :::||||||: ||||||:::||:|||||| |||||
Db   59 ArgProGlyLysGlyLeu---GluTrpIleGlyArgValTyrProGlyAspGlyAspThr 77

Qy   61 ACATACAGCCCGTCCTTCCAAGGC 84
           |||::: ||||||||:::|||
Db   78 AsnTyrAsnGlyLysPheLysGly 85

RESULT 5
HV06_MOUSE
ID   HV06_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01750;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region 102 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: This germline gene belongs to a set of closely
CC   related genes that could encode V regions of NPb antibodies.
DR   PIR; A02032; HVMS02.
DR   PDB; 1QNZ; NMR; H=20-117.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   117   Ig heavy chain V region 102.
FT   DOMAIN   20   49   Framework-1.
FT   DOMAIN   50   54   Complementarity-determining-1.
FT   DOMAIN   55   68   Framework-2.

```
FT   DOMAIN          69     85    Complementarity-determining-2.
FT   DOMAIN          86    117    Framework-3.
FT   DISULFID        41    115    By similarity.
FT   NON_TER        117    117
SQ   SEQUENCE       117 AA;   12867 MW;  740A65DB851FCA8C CRC64;

Alignment Scores:
Pred. No.:                     2.72
Score:                        74.70
Percent Similarity:           60.00%           Length:          117
Best Local Similarity:        43.33%           Matches:          13
Query Match:                  50.47%           Conservative:      5
DB:                            1               Mismatches:        9
                                               Indels:            3
                                               Gaps:              0

NOLAN463-2B.SEQ (1-84) x HV06_MOUSE (1-117)

Qy    1  CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATAACC  60
            |||     ||||||:::  |||||:|||||||||
Db   59  ArgProGlyGlnGlyLeu--GluTrpIleGlyArgIleHisProSerAspSerAspThr  77

Qy   61  ACATACAGCCCGTCCTTCCAAGGC  84
            |||:|||  ||||||||
Db   78  AsnTyrAsnGlnLysPheLysGly  85

RESULT 6
HV52_MOUSE     STANDARD;     PRT;    117 AA.
ID   HV52_MOUSE
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region VH558 A1/A4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; M13787; AAA38499.1; -.
DR   PIR; A02029; HVMSA1.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1     19
FT   CHAIN          20    117    Ig heavy chain V region VH558 A1/A4.
FT   DOMAIN         20     49    Framework-1.
FT   DOMAIN         50     54    Complementarity-determining-1.
FT   DOMAIN         55     68    Framework-2.
FT   DOMAIN         69     85    Complementarity-determining-2.
FT   DOMAIN         86    117    Framework-3.
FT   DISULFID       41    115    By similarity.
FT   NON_TER       117    117
SQ   SEQUENCE      117 AA;   12971 MW;  8B0BC138856DFC9D CRC64;

Alignment Scores:
```

```
Pred. No.:                     2.72
Score:                        74.70
Percent Similarity:           56.67%           Length:          117
Best Local Similarity:        43.33%           Matches:          13
Query Match:                  50.47%           Conservative:      4
DB:                                            Mismatches:       10
                                               Indels:            3
                                               Gaps:              0

NOLAN463-2B.SEQ (1-84) x HV52_MOUSE (1-117)

Qy    1  CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATAACC  60
            |||     ||||||:::  |||::|||||||||
Db   59  ArgProGlyGlnGlyLeu--GluTrpIleGlyTrpIleGlyArgIleTyrProGlySerThr  77

Qy   61  ACATACAGCCCGTCCTTCCAAGGC  84
            |||:|||  ||||||:::|||
Db   78  LysTyrAsnGluLysPheLysGly  85

RESULT 7
Q9JL83
ID   Q9JL83
AC   Q9JL83;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RX   DOI=10.1128/IAI.68.10.5803-5808.2000;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206023; AAF69321.1; -.
DR   HSSP; P01751; INQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1      1
FT   NON_TER      110    110
SQ   SEQUENCE     110 AA;   12052 MW;  84E6F2AD219AF95E CRC64;

Alignment Scores:
Pred. No.:                     3.61
Score:                        73.70
Percent Similarity:           56.67%           Length:          110
Best Local Similarity:        43.33%           Matches:          13
Query Match:                  49.80%           Conservative:      4
DB:                                            Mismatches:       10
                                               Indels:            3
                                               Gaps:              0

NOLAN463-2B.SEQ (1-84) x Q9JL83 (1-110)

Qy    1  CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATAACC  60
            |||     ||||||:::  |||||:|||||||||
Db   32  ArgProGlyGlnGlyLeu--GluTrpIleGlyArgIleTyrProGlyAspAla  50

Qy   61  ACATACAGCCCGTCCTTCCAAGGC  84
            |||:|||  |||||||
Db   51  TyrTyrAsnGlyLysPheLysGly  58

RESULT 8
Q91WT1
ID   Q91WT1
AC   Q91WT1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
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(Left column)

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DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-VJ558 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013490; AAH13490.1; -.
HSSP; P01751; 1A6W.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE  481 AA;  52105 MW;  97DF68D159463F65 CRC64;

Alignment Scores:
Pred. No.:                                    481
Score:                        4.58            Matches:          13
Percent Similarity:          73.70            Conservative:      5
Best Local Similarity:       60.00%           Mismatches:        9
Query Match:                 43.33%           Indels:            3
DB:                          49.80%           Gaps:              0

NOLAN463-2B.SEQ (1-84) x Q91WT1 (1-481)

Qy     1  CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC  60
            ||||||        ||:::         ||||||||||||    :::||
Db    59  ArgProGlyGlnGlyLeu---ValTrpIleGlyTrpProGlyAspGlyAsnThr  77

Qy    61  ACATACAGCCCGTCCTTCCAAGGC  84
            ||::::            ||::::||
Db    78  LysTyrAsnGluLysPheLysGly  85

RESULT 9
Q6PF95
ID   Q6PF95       PRELIMINARY;       PRT;    464 AA.
AC   Q6PF95;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

(Right column)

```
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC057672; AAH57672.1; -.
HSSP; P01865; 1KB5.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE  464 AA;  51096 MW;  5B83746D85A1888 CRC64;

Alignment Scores:
Pred. No.:                                    464
Score:                        6.12            Matches:          13
Percent Similarity:          72.70            Conservative:      5
Best Local Similarity:       60.00%           Mismatches:        9
Query Match:                 43.33%           Indels:            3
DB:                          49.12%           Gaps:              0

NOLAN463-2B.SEQ (1-84) x Q6PF95 (1-464)

Qy     1  CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTTCGATACC  60
            ||||||        |||::::        ||||||||||        |||
Db    59  ArgSerGlyGlnGlyLeu---GluTrpIleAlaArgIleTyrProGlyThrGlySerThr  77

Qy    61  ACATACAGCCCGTCCTTCCAAGGC  84
            ||:::::            |||:::||
Db    78  TyrTyrAsnGluLysPheLysGly  85

RESULT 10
Q99LC4
ID   Q99LC4       PRELIMINARY;       PRT;    463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB   Igh-4 protein.
GN   Name=Igh-4;
```

OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   PIR; B45837; B45837.
DR   HSSP; P01869; 1CL7.
DR   MGD; MGI:96446; Igh-4.
DR   GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR   GO; GO:0003823; F:antigen binding; IDA.
DR   GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR   GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR   GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR   GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR   GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR   GO; GO:0050778; P:positive regulation of immune response; IDA.
DR   GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR   GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR   GO; GO:0001798; P:positive regulation of type IIa hypersensit. . .; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Alignment Scores:
Pred. No.:   8.23
Score: 71.70
Percent Similarity: 56.67%
Best Local Similarity: 43.33%
Query Match: 48.45%
DB: 2

Length: 463
Matches: 13
Conservative: 4
Mismatches: 10
Indels: 3
Gaps: 0

NOLAN463-2B.SEQ (1-84) x Q99LC4 (1-463)

Qy   1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
          || |||||||||::: |||||||||||||||||||| ::: ||
Db   59 ArgThrGlyGlnGlyLeu--GluTrpValGlyIleIleTyrProGlySerGlyAsnThr 77

Qy   61 ACATACAGCCCGTCCTTCCAAGGC 84
          |||||| |||:::||||
Db   78 TyrTyrSerGluLysPheLysGly 85

RESULT 11
HV1F_HUMAN
ID   HV1F_HUMAN   STANDARD;   PRT;   125 AA.
AC   P06326;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-I region Mot.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86203277; PubMed=3084950; DOI=10.1016/0161-5890(86)90039-8;
RA   Kojima M., Koide T., Odani S., Ono T.;
RT   "Amino acid sequence of the variable region of heavy chain in
RT   immunoglobulin (Mot) having unusual papain cleavage sites.";
RL   Mol. Immunol. 23:169-174(1986).
DR   PIR; A02025; HVHUMO.
DR   HSSP; P01751; 1A6W.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN   1   98   V segment.
FT   DOMAIN   99   107   D segment.
FT   DOMAIN   108   125   J segment.
FT   DISULFID   22   96   By similarity.
FT   NON_TER   125   125
SQ   SEQUENCE   125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Alignment Scores:
Pred. No.:   18.7
Score: 68.20
Percent Similarity: 53.12%
Best Local Similarity: 37.50%
Query Match: 46.08%
DB: 1

Length: 125
Matches: 12
Conservative: 5
Mismatches: 7
Indels: 8
Gaps: 0

NOLAN463-2B.SEQ (1-84) x HV1F_HUMAN (1-125)

Qy   2 GGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACCA 61
          |||||| |||:::: ::||||||||::|||::::|||::||:::||| ||||
Db   42 GlyArg-----GlyLeu--GluTrpMetAlaValHisProSerAspAspArgThr 59

RESULT 12
HV05_MOUSE
ID   HV05_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01749;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V region 3 precursor.
GN   Name=Igh-V5558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]

Qy   62 CATACAGCCCGTCCTTCCAA 81
          |||||| |||||||
Db   59 hrTyrGlyProArgSerGln 65

RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: This germline gene belongs to a set of closely
CC   related genes that could encode v regions of NPb antibodies.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; J00536; AAA38605.1; -.
DR   PIR; A02031; HVMS3.
DR   HSSP; P01810; 2FBJ.
DR   MGD; MGI:96486; Igh-VU558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig;1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   117   Ig heavy chain V region 3.
FT   DOMAIN   20   49   Framework-1.
FT   DOMAIN   50   54   Complementarity-determining-1.
FT   DOMAIN   55   68   Framework-2.
FT   DOMAIN   69   85   Complementarity-determining-2.
FT   DOMAIN   86   117   Framework-3.
FT   DISULFID   41   115   By similarity.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA;   13016 MW;   427C861C53975EDC CRC64;

Alignment Scores:
Pred. No.:   Length: 117
Score: 21.5   Matches: 12
Percent Similarity: 67.70%   Conservative: 5
Best Local Similarity: 58.62%   Mismatches: 9
Query Match: 41.38%   Indels: 3
DB: 45.74%   Gaps: 0

NOLAN463-2B.SEQ (1-84) x HV05_MOUSE (1-117)

Qy   1 CGGGCGAGTCAGGGTATTAGCAGCAGTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
        ||| |||||||||::: ||||:|| ||||||||| ||||||||::|||||
Db   59 ArgProGlyGlnGlyLeu--GluTrpIleGlyAsnIleTyrProSerAspSerGluThr 77

Qy   61 ACATACAGCCCGTCCTTCCAA 81
        |||:|| |||:|||
Db   78 HisTyrAsnGlnLysPheLys 84

RESULT 13
Q91V67
ID   Q91V67   PRELIMINARY;   PRT;   143 AA.
AC   Q91V67;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN   Name=VH186.2-D-J-C mu; Synonyms=v304-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069912; BAB63928.1; -.
DR   EMBL; AB069914; BAB63930.1; -.
DR   PIR; S26744; S26744.
DR   HSSP; P01751; 1A6W.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   143   143
SQ   SEQUENCE   143 AA;   15775 MW;   91BC6012B44EFBBF CRC64;

Alignment Scores:
Pred. No.:   Length: 143
Score: 29.8   Matches: 12
Percent Similarity: 66.70%   Conservative: 5
Best Local Similarity: 56.67%   Mismatches: 10
Query Match: 40.00%   Indels: 3
DB: 45.07%   Gaps: 0

NOLAN463-2B.SEQ (1-84) x Q91V67 (1-143)

Qy   1 CGGGCGAGTCAGGGTATTAGCAGCAGTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
        ||| |||||||::: ||||:|| ||||||| ::||| |||||:|||||
Db   40 ArgProGlyGlnGlyLeu--GluTrpIleGlyValIleAspProSerAspSerTyrThr 58

Qy   61 ACATACAGCCCGTCCTTCCAAGGC 84
        |||:|| |||:||||
Db   59 AsnTyrAsnGlnLysPheLysGly 66

RESULT 14
Q6GMX8
ID   Q6GMX8   PRELIMINARY;   PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.

```
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8B14B6559EFC9 CRC64;

Alignment Scores:
Pred. No.:                   46.1        Length:            236
Score:                       65.50       Matches:            14
Percent Similarity:          36.36%      Conservative:        2
Best Local Similarity:       31.82%      Mismatches:          3
Query Match:                 44.26%      Indels:             25
DB:                          2           Gaps:                0

NOLAN463-2B.SEQ (1-84) x Q6GMX8 (1-236)

Qy    1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
         |||||||||||||||||||||||||||||||||||||||     ||
Db   46 ArgAlaSerGlnGlyIleSerSerTrpLeuAla---------Trp------------- 57

Qy   61 ACATACAGCCCGTCCTTCCAAG 82
         ::: ::|||  |||
Db   58 -TyrGlnGlnLysProGlyLys 64

RESULT 15
Q7TPE3
ID   Q7TPE3        PRELIMINARY;      PRT;  136 AA.
AC   Q7TPE3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   V23-D-J-IgG1 protein (Fragment).
GN   Name=V23-D-J-IgG1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuna T.;
RT   "The higher density hapten Ag stimulates strong signal to B cells.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069864; BAC54573.1; -.
HSSP; P01751; 1A6V.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  14882 MW;  99392B1A31F663AF CRC64;

Alignment Scores:
Pred. No.:                   53.5        Length:            136
Score:                       64.70       Matches:            11
Percent Similarity:          55.17%      Conservative:        5
Best Local Similarity:       37.93%      Mismatches:         10
Query Match:                 43.72%      Indels:              3
DB:                          2           Gaps:                0

NOLAN463-2B.SEQ (1-84) x Q7TPE3 (1-136)

Qy    1 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCATCATCTATCCTGGTGACTCTGATACC 60
```

```
Db        |||
     37 ArgProGlyGlnGlyLeu--GluTrpIleGlyAsnIleTyrProSerAsnGlyAspThr 55
```

```
Qy   61 ACATACAGCCCGTCCTTCCAA 81
         ||:::    |||:::
Db   56 AsnTyrAsnGluLysPheLys 62
```

Search completed: August 4, 2005, 19:01:29
Job time : 85.75 secs

```
            GenCore version 5.1.6
      Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August  4, 2005, 19:02:48 ; Search time 114 Seconds
                                       (without alignments)
                            549.607 Million cell updates/sec

Title:          DELETED1
Perfect score:  140
Sequence:       1 GAAATCAATCATAGTGGAAG.........ATATTAGCAGCTCGTTAGCC 81

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.1
                Ygapop 10.0 , Xgapext  0.1
                Fgapop  6.0 , Fgapext  0.1
                Delop   6.0 , Delext   0.1

Searched:       2105692 seqs, 38676381 residues

Total number of hits satisfying chosen parameters:      4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3A/runat_04082005_120124_18790/app_query.fasta_1.263
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3A_@CGN_1_1_224 @runat_04082005_120124_18790 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=1 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :  A_Geneseq_16Dec04:*
         1: geneseqp1980s:*
         2: geneseqp1990s:*
         3: geneseqp2000s:*
         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2003as:*
         7: geneseqp2003bs:*
         8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	113.1	80.8	249	5	ABP45310	Abp45310 Human BLy
2	113.1	80.8	249	7	ADG96137	Adg96137 Single ch
3	93.8	67.0	250	5	ABP44982	Abp44982 Human BLy
4	93.8	67.0	250	7	ADG95809	Adg95809 Single ch
5	93.8	67.0	253	5	ABP44943	Abp44943 Human BLy
6	93.8	67.0	253	7	ADG95770	Adg95770 Single ch
7	92.4	66.0	80	2	AAW62794	Aaw62794 Amino aci
8	92.4	66.0	97	5	AAY05694	Aay05694 Multiple
9	92.4	66.0	97	5	ABG78212	Abg78212 Human Fv
10	92.4	66.0	97	5	ABG91903	Abg91903 Human ant
11	92.4	66.0	97	6	ABO27107	Abo27107 Human ger
12	92.4	66.0	97	7	ADB75646	Adb75646 Human pro
13	92.4	66.0	97	7	ADD28104	Add28104 Lymphoma
14	92.4	66.0	97	7	ADF10048	Adf10048 VEGF anti
15	92.4	66.0	97	7	ADF10150	Adf10150 Antibody
16	92.4	66.0	97	7	ADF09942	Adf09942 Antibody
17	92.4	66.0	97	7	ADJ80323	Adj80323 VH gene 1
18	92.4	66.0	114	3	AAB01949	Aab01949 Anti-Id1
19	92.4	66.0	114	3	AAB01950	Aab01950 Anti-Id1
20	92.4	66.0	114	3	AAB01953	Aab01953 Anti-Id1
21	92.4	66.0	114	3	AAB01959	Aab01959 High affi
22	92.4	66.0	114	3	AAB01952	Aab01952 Anti-Id1
23	92.4	66.0	114	3	AAB01955	Aab01955 Strepativ
24	92.4	66.0	114	3	AAB01956	Aab01956 Strepativ
25	92.4	66.0	114	3	AAB01948	Aab01948 Wild-type
26	92.4	66.0	114	7	ADG70086	Adg70086 Diversifi
27	92.4	66.0	114	7	ADG70013	Adg70013 Diversifi
28	92.4	66.0	116	2	AAR66324	Aar66324 Human imm
29	92.4	66.0	117	4	AAM60904	Aam60904 Human bra
30	92.4	66.0	117	5	ABG55317	Abg55317 Human liv
31	92.4	66.0	117	5	ABG43454	Abg43454 Human pep
32	92.4	66.0	118	6	ADA89246	Ada89246 Human ant
33	92.4	66.0	122	7	ADK17418	Adk17418 Anti-huma
34	92.4	66.0	122	8	ADG42840	Adg42840 scFv Ab12
35	92.4	66.0	123	2	AAW03757	Aaw03757 Anti-rhes
36	92.4	66.0	125	6	ADA89266	Ada89266 Human ant
37	92.4	66.0	125	6	ADA89274	Ada89274 Human ant
38	92.4	66.0	139	3	AAY99556	Aay99556 Human LH1
39	92.4	66.0	139	7	ABR42859	Abr42859 Tumour-sp
40	92.4	66.0	139	7	ABW02445	Abw02445 Human mon
41	92.4	66.0	142	6	ABP96287	Abp96287 Anti-hTNF
42	92.4	66.0	154	6	ABP96293	Abp96293 Human ant
43	92.4	66.0	190	2	AAY34304	Aay34304 Human ant
44	92.4	66.0	202	2	AAY34303	Aay34303 IgM antib
45	92.4	66.0	205	2	AAY34299	Aay34299 IgM antib

ALIGNMENTS

```
RESULT 1
ABP45310
ID   ABP45310 standard; protein; 249 AA.
XX
AC   ABP45310;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1321.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
```

```
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1979-1980; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 249 AA;

Alignment Scores:
Pred. No.:                8.88e-06        Length:              249
Score:                    113.10          Matches:             26
Percent Similarity:       20.63%          Conservative:        0
Best Local Similarity:    20.63%          Mismatches:          1
Query Match:              80.79%          Indels:              99
DB:                       5               Gaps:                1

DELETED1 (1-81) x ABP45310 (1-249)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGT------------ 48
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 ---------------------------------------------------------- 48
Db   70 SerValAspThrSerLysAsnGlnPheSerLeuLeuSerSerValThrAlaAlaAsp 89

Qy   48 ---------------------------------------------------------- 48
Db   90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109

Qy   48 ---------------------------------------------------------- 48
Db  110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129

Qy   48 ---------------------------------------------------------- 48
Db  130 GlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149

Qy   49 --------------------------------------CGGGCGAGTCAGGAT 63
                                              |||||||||||||||
Db  150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169

Qy   64 ATTAGCAGCTGGTTAGCC 81
        ||||||||||||
Db  170 IleSerSerTrpLeuAla 175
```

RESULT 2
ADG96137
ID   ADG96137 standard; protein; 249 AA.
XX
AC   ADG96137;
XX

```
DT   11-MAR-2004  (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 1321.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO200305979-A2.
XX
PD   10-JUL-2003.
XX
PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 1321; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ   Sequence 249 AA;

Alignment Scores:
Pred. No.:                8.88e-06        Length:              249
Score:                    113.10          Matches:             26
Percent Similarity:       20.63%          Conservative:        0
Best Local Similarity:    20.63%          Mismatches:          1
Query Match:              80.79%          Indels:              99
DB:                       7               Gaps:                1

DELETED1 (1-81) x ADG96137 (1-249)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGT------------ 48
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 ---------------------------------------------------------- 48
```

```
Db  70 SerValAspThrSerLysAsnGlnPheSerLeuLysSerSerValThrAlaAlaAsp 89
Qy  48 -------------------------------------------------------- 48
Db  90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
Qy  48 ------------------------------------------------------------ 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
Qy  48 ------------------------------------------------------------ 48
Db 130 GlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
Qy  49 ------------------------------------------------CGGGCGAGTCAGGAT 63
                                                         ||||||||||||
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
Qy  64 ATTAGCAGCTGGTTAGCC 81
        ||||||||||||||||||
Db 170 IleSerSerTrpLeuAla 175


RESULT 3
ABP44982
ID   ABP44982 standard; protein; 250 AA.
XX
AC   ABP44982;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 993.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1586-1587; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 250 AA;

Alignment Scores:
Pred. No.:               0.00327       Length:         250
Score:                   93.80         Matches:         20
Percent Similarity:      80.77%        Conservative:     1
Best Local Similarity:   76.92%        Mismatches:       3
Query Match:             67.00%        Indels:           2
DB:                      5             Gaps:             1

DELETED1 (1-81) x ABP44982 (1-250)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGCG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||  |||||
Db  50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnProSerArgValThrIle 69

Qy  55 AGTCAGGATATTAGCCAGC 72
        |||||||||  ||:::
Db  70 SerGlnAspThrSerAsn 75


RESULT 4
ADG95809
ID   ADG95809 standard; protein; 250 AA.
XX
AC   ADG95809;
XX
DT   11-MAR-2004 (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 993.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO200305979-A2.
XX
PD   10-JUL-2003.
XX
PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 993; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 11q34 and encodes a protein that is a member of the tumour
```

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CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ   Sequence 250 AA;

Alignment Scores:
Pred. No.:              0.00327        Length:         250
Score:                 93.80          Matches:         20
Percent Similarity:    80.77%         Conservative:     1
Best Local Similarity: 76.92%         Mismatches:       3
Query Match:           67.00%         Indels:           2
DB:                    7              Gaps:             1

DELETED1 (1-81) x ADG95809 (1-250)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAAGAGTCGGGCG------  54
         ||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle  69

Qy   55 AGTCAGGATATTAGCAGC  72
         ||||||||||  |||:::
Db   70 SerGlnAspThrSerAsn  75

RESULT 5
ABP44943
ID   ABP44943 standard; protein; 253 AA.
XX
AC   ABP44943;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 954.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO20020641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
```

```
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1540-1541; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 253 AA;

Alignment Scores:
Pred. No.:              0.00328        Length:         253
Score:                 93.80          Matches:         20
Percent Similarity:    80.77%         Conservative:     1
Best Local Similarity: 76.92%         Mismatches:       3
Query Match:           67.00%         Indels:           2
DB:                    5              Gaps:             1

DELETED1 (1-81) x ABP44943 (1-253)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTTCAAGAGTCGGGCG------  54
         ||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle  69

Qy   55 AGTCAGGATATTAGCAGC  72
         ||||||||||  |||:::
Db   70 SerGlnAspThrSerAsn  75

RESULT 6
ADG95770
ID   ADG95770 standard; protein; 253 AA.
XX
AC   ADG95770;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 954.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2003055979-A2.
XX
PD   10-JUL-2003.
XX
PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
```

```
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 954; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis; inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ   Sequence 253 AA;

Alignment Scores:
Pred. No.:             0.00328          Length:          253
Score:                 93.80%           Matches:         20
Percent Similarity:    80.77%           Conservative:    1
Best Local Similarity: 76.92%           Mismatches:      3
Query Match:           67.00%           Indels:          2
DB:                    7                Gaps:            1

DELETED1 (1-81) x ADG95770 (1-253)

Qy    1 GAAATCAATCATATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG------ 54
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db   50 GluIleAsnHisSerGlySerThrThrArgProSerLeuAsnSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
         ||||||||  |||:::
Db   70 SerGlnAspThrSerAsn 75


RESULT 7
AAW62794
ID   AAW62794 standard; peptide; 80 AA.
XX
AC   AAW62794;
XX
DT   23-SEP-1998  (first entry)
XX
DE   Amino acid sequence of a human antibody fragment.
XX
KW   Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW   inactivated endogenous Ig locus; B-cell development;
KW   human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW   kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW   production; antibody.
XX
```

```
OS   Homo sapiens.
XX
PN   WO9824893-A2.
XX
PD   11-JUN-1998.
XX
PF   03-DEC-1997;  97WO-US023091.
XX
PR   03-DEC-1996;  96US-00759620.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX
DR   WPI; 1998-333314/29.
XX
PT   New transgenic non-human mammals - having an inactivated immunoglobulin
PT   locus and a near complete human immunoglobulin locus, used for production
PT   of human antibodies.
XX
PS   Disclosure; Page 71; 128pp; English.
XX
CC   AAW62793-822 represent fragments of human antibodies produced by
CC   transgenic Xenomice, created using the method of the invention. The
CC   specification describes a transgenic non-human mammal which has genome
CC   modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC   locus, so that the mammal does not display normal B-cell development. The
CC   modified genome also has an inserted human heavy chain Ig locus in
CC   germline configuration, the human heavy chain Ig locus comprising a human
CC   micro constant region and regulatory and switch sequences, human J-H
CC   genes, human D-H genes, and human V-H genes and an inserted human kappa
CC   light chain Ig locus in germline configuration, the human kappa light
CC   chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC   and V-kappa genes, where the number of V-H and V-kappa genes inserted are
CC   selected to restore normal B-cell development in the mammal. The
CC   transgenic animals have a near complete human Ig locus, including both a
CC   human heavy chain locus and a human kappa light chain locus. They can be
CC   used for the production of human antibodies when exposed to particular
CC   antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC   will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
SQ   Sequence 80 AA;

Alignment Scores:
Pred. No.:             0.00354          Length:          80
Score:                 92.40            Matches:         19
Percent Similarity:    74.07%           Conservative:    1
Best Local Similarity: 70.37%           Mismatches:      1
Query Match:           66.00%           Indels:          6
DB:                    2                Gaps:            0

DELETED1 (1-81) x AAW62794 (1-80)

Qy    1 GAAATCAATCATATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   33 GluIleAsnHisSerGlySerThrThrAsnProSerLeuLysSerArgValThr--- 51

Qy   61 GATATTAGC 69
         ||||||
Db   52 ---IleSer 53


RESULT 8
AAY05694
ID   AAY05694 standard; protein; 97 AA.
XX
AC   AAY05694;
XX
DT   19-JUL-1999  (first entry)
XX
DE   Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
XX
KW   Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
KW   heavy chain variable region; VH gene; somatic hypermutation;
XX
```

```
KW  B-cell clonality; RA gene; diagnosis; human.
XX
OS  Homo sapiens.
XX
FH  Key              Location/Qualifiers
FT  Region           1..30
FT                   /label= FR1
FT  Misc-difference  8
FT                   /note= "encoded by GGC"
FT  Misc-difference  13
FT                   /note= "replaces Glu of RA"
FT  Misc-difference  14
FT                   /note= "encoded by CCT"
FT  Misc-difference  23
FT                   /note= "replaces Gly of RA"
FT  Misc-difference  25
FT                   /note= "replaces Phe of RA"
FT  Misc-difference  30
FT                   /note= "replaces Gly of RA"
FT  Region           31..36
FT                   /label= CDR1
FT  Misc-difference  31
FT                   /note= "replaces Gly of RA"
FT  Misc-difference  32
FT                   /note= "replaces Phe of RA"
FT  Region           37..50
FT                   /label= FR2
FT  Region           51..66
FT                   /label= CDR2
FT  Misc-difference  56
FT                   /note= "replaces Asn of RA"
FT  Misc-difference  57
FT                   /note= "replaces Ser of RA"
FT  Misc-difference  58
FT                   /note= "replaces Lys of RA"
FT  Region           67..97
FT                   /label= FR3
FT  Misc-difference  71
FT                   /note= "replaces Leu of RA"
FT  Misc-difference  81
FT                   /note= "replaces Arg of RA"
XX
PN  WO9915696-A1.
XX
PD  01-APR-1999.
XX
PF  17-SEP-1998;  98WO-CA000873.
XX
PR  19-SEP-1997;  97CA-02216595.
PR  04-NOV-1997;  97CA-02222245.
XX
PA  (QINY/) QIN Y.
XX
PI  Qin Y;
XX
DR  WPI; 1999-276985/23.
DR  N-PSDB; AAX25318.
XX
PT  Determination of B-cell clonality by amplification or enzymatic
PT  digestion.
XX
PS  Disclosure; Fig 9D; 67pp; English.
XX
CC  This sequence represents a heavy chain variable region (VH) as predicted
CC  from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
CC  fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
CC  B-cells were obtained from 4 MS patients (see AAX25516-19). Differences
CC  in nucleotide and predicted amino acid (see AAY05691-94) sequences were
CC  compared with the closest known germline VH genes; for 4d76, this was RA.
CC  The results provided direct evidence that intrathecal clonally expanded B
CC  -cells from the CSF of MS patients are hypermutated postgerminal centre
CC  antibody-forming or memory lymphocytes that have undergone antigen
CC  selection. This finding implicates an important pathogenic pathway for
CC  the development of demyelination in CNS of MS. The invention provides
CC  assay kits for determining B-cell or T-cell clonality. This technology
CC  allows the establishment of clonal specific RNA library from pathogenic
CC  cells in the CNS of patients, which is important for further
CC  understanding of the role of antigen(s) in the cause of B-cell clonal
CC  expansion, and towards developing antigen specific therapeutic strategy
XX
SQ  Sequence 97 AA;

Alignment Scores:
Pred. No.:                         Length:        97
Score:                 0.00375     Matches:       19
Percent Similarity:    92.40       Conservative:  1
Best Local Similarity: 74.07%      Mismatches:    1
Query Match:           70.37%      Indels:        6
DB:                    66.00%      Gaps:          0
                       2

DELETED1 (1-81) x AAY05694 (1-97)

Qy    1  GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTTCAAGAGTCGGGCGAGTCAG  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db   50  GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy   61  GATATTAGC  69
         |||||
Db   69  ---IleSer  70

RESULT 9
ABG78212
ID   ABG78212 standard; protein; 97 AA.
XX
AC   ABG78212;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human Fv molecule hypervariable region related peptide #87.
XX
KW   Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW   disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW   lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200259264-A2.
XX
PD   01-AUG-2002.
XX
PF   31-DEC-2001; 2001WO-US049440.
XX
PR   29-DEC-2000; 2000US-00751181.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI   Plaksin D, Peretz T;
XX
DR   WPI; 2002-619166/66.
XX
PT   Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT   or fragment, or construct of fragment with enhanced binding
PT   characteristics so as to selectively bind target cell in favor of other
PT   cells.
XX
PS   Claim 13; Page 193; 232pp; English.
XX
CC   The invention relates to a peptide or polypeptide comprising an Fv
CC   molecule, a construct or fragments or a construct of a fragment with
CC   enhanced binding characteristics which selectively and/or specifically
CC   binds to a target cell in favour of other cells, where binding is
CC   primarily determined by a first hypervariable region and Fv is a single
CC   chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC   association with or attached, coupled, combined, linked or fused to a
CC   pharmaceutical agent, is useful in the manufacture of a medicament, where
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CC   the medicament has activity against a diseased cell, preferably a cancer
CC   cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC   myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC   acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC   composition for use in inhibiting the growth of a diseased or cancer
CC   cell. This sequence represents a human Fv molecule hypervariable region
CC   related peptide of the invention
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:             0.00375       Length:          97
Score:                 92.40         Matches:         19
Percent Similarity:    74.07%        Conservative:    1
Best Local Similarity: 70.37%        Mismatches:      1
Query Match:           66.00%        Indels:          6
DB:                    5             Gaps:            0

DELETED1 (1-81) x ABG78212 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        |||||
Db   69 ---IleSer 70

RESULT 10
ABG91903
ID   ABG91903 standard; protein; 97 AA.
XX
AC   ABG91903;
XX
DT   04-DEC-2002 (first entry)
XX
DE   Human antibody fragment #87.
XX
KW   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW   metastasis; hypervariable region; autoimmune disease; thrombosis;
KW   restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW   myocardial infarction; retinopathic disease; abnormal platelet function;
KW   sulphated tyrosine-dependent protein-protein interaction.
XX
OS   Homo sapiens.
XX
PN   WO200253700-A2.
XX
PD   11-JUL-2002.
XX
PF   31-DEC-2001; 2001WO-US049442.
XX
PR   29-DEC-2000; 2000US-00751181.
PR   29-DEC-2000; 2000US-0258948P.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI   Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR   WPI; 2002-674776/72.
XX
PT   Novel isolated epitope present on cancer cells and important in
PT   physiological phenomena such as cell rolling, metastasis and
PT   inflammation, for treating autoimmune, inflammatory or cardiovascular
PT   diseases, and cancer.
XX
PS   Disclosure; Page 269; 0pp; English.
XX
CC   The invention relates to an isolated epitope present on cancer cells and
CC   important in physiological phenomena such as cell rolling, metastasis and
CC   inflammation, where the epitope is capable of being bound by an antibody,
CC   its antigen-binding fragment or its complex comprising at least one
```

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CC   antibody or its binding fragment having a first hypervariable region. The
CC   epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC   disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC   tumour or leukaemia cells, increase in number of tumour or leukaemia
CC   cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC   platelet and/or cell-platelet adhesion or aggregation, for increasing
CC   mortality of tumour or leukaemia cells, for increasing the susceptibility
CC   of diseased cells to damage by anti-disease, anti-cancer or anti-
CC   leukaemia agents, or for decreasing the number of tumour or leukaemia
CC   cells in a patient, or in the manufacture of a medicament for the above
CC   mentioned purposes. The epitopes are useful for diagnosing and treating
CC   diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC   diseases, cardiovascular diseases such as myocardial infarction,
CC   retinopathic diseases and other diseases mediated by abnormal platelet
CC   function and diseases caused by sulphated tyrosine-dependent protein-
CC   protein interactions. This sequence represents a human antibody fragment
CC   of the invention
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:             0.00375       Length:          97
Score:                 92.40         Matches:         19
Percent Similarity:    74.07%        Conservative:    1
Best Local Similarity: 70.37%        Mismatches:      1
Query Match:           66.00%        Indels:          6
DB:                    5             Gaps:            0

DELETED1 (1-81) x ABG91903 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        |||||
Db   69 ---IleSer 70

RESULT 11
ABO27107
ID   ABO27107 standard; protein; 97 AA.
XX
AC   ABO27107;
XX
DT   10-SEP-2003 (first entry)
XX
DE   Human germline heavy chain variable region gene segment #40.
XX
KW   Human; heavy chain variable region; VH; humanised antibody;
KW   chimeric antibody; complementarity determining region; CDR;
KW   canonical CDR structure type.
XX
OS   Homo sapiens.
XX
PN   US2003039649-A1.
XX
PD   27-FEB-2003.
XX
PP   12-JUL-2002; 2002US-00194975.
XX
PR   12-JUL-2001; 2001US-0305111P.
XX
PA   (FOOT/) FOOTE J.
XX
PI   Foote J;
XX
DR   WPI; 2003-492151/46.
XX
PT   Making humanized antibody for converting antibody, by making chimeric
PT   antibodies containing complementarity determining region from non-human
PT   antibody and appropriate framework sequences of human antibodies.
XX
PS   Example 1; Fig 1; 31pp; English.
```

XX
CC   The invention describes a method of making a humanised antibody,
CC   comprising making chimeric antibodies containing a complementarity
CC   determining region (CDR) from a non-human antibody and appropriate
CC   framework sequences (I) of human antibodies. (I) is selected by using
CC   canonical CDR structure types of non-human antibody in comparison to
CC   germline canonical CDR structure types of human antibodies as the basis
CC   for selection, for humanisation. The method is useful for making a
CC   humanised antibody or a converted antibody. The method is applicable for
CC   converting a subject antibody sequence of any subject species to a less
CC   immunogenic form suitable for use in an object species. The method is
CC   reliable for identifying suitable human framework sequences to support
CC   non-human CDR regions and to provide humanised antibodies that retain
CC   high antigen binding with low immunogenicity in humans, without the need
CC   for direct comparison of framework sequences, without the need for
CC   determining critically important amino acid residues in the framework,
CC   and without the need for multiple iteration and construction to obtain
CC   humanised antibodies with suitable therapeutic properties. The antibody
CC   has high affinity and low immunogenicity without need for comparing
CC   framework sequences between non-human and human antibodies. This sequence
CC   represents a human heavy chain variable region gene segment used in the
CC   creation of humanised antibodies
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00375   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 6   Gaps: 0

DELETED1 (1-81) x ABO27107 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        |||||||||||||||||||||||||||||| ||| ||:|||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        ||||||
Db   69 ---IleSer 70

RESULT 12
ADB75646
ID   ADB75646 standard; protein; 97 AA.
XX
AC   ADB75646;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human protein relating to the invention SEQ ID NO:55.
XX
KW   antibody library; CD1 region; CD2 region; VH region; VL region;
KW   immunoglobulin; CD3 region; TM1 scFv; human.
XX
OS   Homo sapiens.
XX
PN   WO200304198-A1.
XX
PD   30-MAY-2003.
XX
PF   22-NOV-2002; 2002WO-JP012236.
XX
PR   22-NOV-2001; 2001JP-00358602.
XX
PA   (UYKE-) UNIV KEIO.
XX
PI   Shimizu N, Takayanagi A, Okui M;
XX
DR   WPI; 2003-449818/42.
XX
PT   Highly stable artificial antibody libraries with super-repertory and

PT   little contamination from unexpressible ones, useful as tool in
PT   proteomics and e.g. for diagnosis and treating various diseases.
XX
PS   Disclosure; Page 101; 108pp; Japanese.
XX
CC   The invention relates to a novel artificial single-stranded antibody
CC   library with superior-repertory. The library is created by using a cDNA
CC   library as template for amplifying a fragment containing the CD1 and CD2
CC   regions of the VH or VL region of immunoglobulin gene and a fragment
CC   containing the CD3 region by PCR, respectively, producing VH and VL
CC   libraries, transferring into a host, and displaying the single-stranded
CC   antibody on a phage surface. An antibody library of the invention is
CC   useful as a tool in proteomics and antibody chips and filters, for
CC   screening ligands for antigens, and for studying protein-DNA interaction,
CC   diagnosis and treating various diseases. The present sequence represents
CC   a protein of the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00375   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 7   Gaps: 0

DELETED1 (1-81) x ADB75646 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        |||||||||||||||||||||||||||||| ||| ||:|||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
        ||||||
Db   69 ---IleSer 70

RESULT 13
ADD28104
ID   ADD28104 standard; protein; 97 AA.
XX
AC   ADD28104;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Lymphoma related immunoglobulin variable region F5.
XX
KW   B-cell; malignant; immunoglobulin; immunoglobulin variable region;
KW   Ig variable region; glycosylation site; lymphoma; B cell receptor;
KW   cytostatic; gene therapy; glycosylation inhibitor;
KW   non-Hodgkin's lymphoma.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200307459-A2.
XX
PD   12-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-GB000783.
XX
PR   07-MAR-2002; 2002GB-00005395.
XX
PA   (CANC-) CANCER RES TECHNOLOGY LTD.
XX
PI   Zhu D, Stevenson F;
XX
DR   WPI; 2003-902720/82.
XX
PT   Classifying a B-cell as malignant or normal by isolating a sequence
PT   representing an Ig variable region from the B cell, detecting the
PT   presence of a glycosylation site and classifying the cell as malignant or
PT   normal.

```
XX
PS   Disclosure; Fig 4; 61pp; English.
XX
CC   The present invention describes a method for classifying a B-cell as
CC   malignant or normal comprising: (a) isolating a sequence representing an
CC   immunoglobulin (Ig) variable region from the B cell; (b) detecting the
CC   presence of a glycosylation site; and (c) classifying the cell as
CC   malignant or normal on the basis of the presence or absence of a
CC   glycosylation site. Also described: (1) treating a patient suffering from
CC   or at risk of having lymphoma; (2) screening for substances capable of
CC   inhibiting glycosylation of the Ig variable region of the B cell receptor
CC   ; and (3) screening for substances (S) capable of inhibiting the
CC   interaction between lectins of the type found in the germinal centre and
CC   N-glycans found on the surface of Ig of lymphoma cells. (S) has
CC   cytostatic activity, and can be used in gene therapy, and as a
CC   glycosylation inhibitor. The method is useful in classifying a B-cell as
CC   malignant or normal. The glycosylation inhibitor is useful in preparing a
CC   medicament for treating non-Hodgkin's lymphoma. The present sequence
CC   represents an Ig variable region sequence which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:                0.00375      Length:           97
Score:                    92.40        Matches:          19
Percent Similarity:       74.07%       Conservative:     1
Best Local Similarity:    70.37%       Mismatches:       1
Query Match:              66.00%       Indels:           6
DB:                       7            Gaps:             0

DELETED1 (1-81) x ADD28104 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 14
ADF10048
ID   ADF10048 standard; protein; 97 AA.
XX
AC   ADF10048;
XX
DT   12-FEB-2004  (first entry)
XX
DE   VEGF antibody heavy chain variable region VH_4-34.
XX
KW   Antibody; stability; solubility; antigen binding affinity;
KW   variable region; human; VEGF.
XX
OS   Homo sapiens.
XX
PN   WO2003074679-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
PS   Example 6; Fig 16a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:                0.00375      Length:           97
Score:                    92.40        Matches:          19
Percent Similarity:       74.07%       Conservative:     1
Best Local Similarity:    70.37%       Mismatches:       1
Query Match:              66.00%       Indels:           6
DB:                       7            Gaps:             0

DELETED1 (1-81) x ADF10048 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 15
ADF10150
ID   ADF10150 standard; protein; 97 AA.
XX
AC   ADF10150;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Antibody heavy chain variable region VH_4-34.
XX
KW   Antibody; stability; solubility; antigen binding affinity;
KW   variable region; human.
XX
OS   Homo sapiens.
XX
PN   WO2003074679-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
```

PS   Example 16; Fig 40a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.00375   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 7   Gaps: 0

DELETED1 (1-81) x ADF10150 (1-97)

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Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          ||||||
Db   69 ---IleSer 70

Search completed: August 4, 2005, 19:34:16
Job time : 120 secs

OM nucleic - protein search, using frame_plus_n2p model

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GenCore version 5.1.6

Run on: August 4, 2005, 19:25:09 ; Search time 30 seconds
(without alignments)
403.105 Million cell updates/sec

Title: DELETED1
Perfect score: 140
Sequence: 1 GAAATCAATCATAGTGGAAG.........ATATTAGCAGCTGGTTAGCC 81

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop   6.0 , Delext 0.1

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3A/runat_04082005_120126_18820/app_query.fasta_1.263
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	92.4	66.0	116	3	US-08-545-809A-118	Sequence 118, App
2	92.4	66.0	123	3	US-08-793-450-4	Sequence 4, Appli
3	92.4	66.0	139	4	US-09-203-768A-2	Sequence 2, Appli
4	92.4	66.0	472	3	US-08-793-450-8	Sequence 8, Appli
5	87.4	62.4	429	4	US-09-372-425A-6	Sequence 6, Appli
6	84.4	60.3	118	3	US-09-025-769B-25	Sequence 25, Appl
7	84.4	60.3	118	4	US-09-490-070A-25	Sequence 25, Appl
8	84.4	60.3	118	4	US-09-490-153-25	Sequence 25, Appl
9	84.4	60.3	118	4	US-09-490-324-25	Sequence 25, Appl
10	81	57.9	120	3	US-08-545-809A-137	Sequence 137, App
11	80.7	57.6	130	3	US-08-466-151-5	Sequence 5, Appli
12	80.7	57.6	130	3	US-08-466-163B-5	Sequence 5, Appli
13	80.7	57.6	130	4	US-09-802-096-5	Sequence 5, Appli
14	80.7	57.6	130	4	US-09-802-077-5	Sequence 5, Appli
15	79.4	56.7	147	4	US-09-471-276-835	Sequence 835, App
16	79.4	56.7	447	2	US-09-372-425A-2	Sequence 2, Appli
17	77	55.0	119	2	US-08-428-197-16	Sequence 16, Appl
18	77	55.0	119	5	PCT-US93-10555-16	Sequence 16, Appl
19	76.4	54.6	112	3	US-09-344-587-14	Sequence 14, Appl
20	75.9	54.2	118	2	US-08-652-816A-13	Sequence 13, Appl
21	74.4	53.1	120	4	US-09-424-840B-20	Sequence 20, Appl
22	73.4	52.4	21	3	US-08-918-148-45	Sequence 45, Appl
23	73.4	52.4	21	3	US-09-138-091A-45	Sequence 45, Appl
24	73.4	52.4	76	3	US-08-851-362D-22	Sequence 22, Appl
25	73.4	52.4	96	3	US-08-851-362D-35	Sequence 35, Appl
26	73.4	52.4	116	3	US-08-851-809A-140	Sequence 140, App
27	73.4	52.4	117	3	US-08-851-362D-48	Sequence 48, Appl
28	73.4	52.4	118	3	US-08-545-809A-142	Sequence 142, App
29	73.4	52.4	119	3	US-09-025-769B-39	Sequence 39, Appl
30	73.4	52.4	119	3	US-09-025-769B-65	Sequence 65, Appl
31	73.4	52.4	119	4	US-09-490-070A-39	Sequence 39, Appl
32	73.4	52.4	119	4	US-09-490-070A-65	Sequence 65, Appl
33	73.4	52.4	119	4	US-09-490-153-39	Sequence 39, Appl
34	73.4	52.4	119	4	US-09-490-153-65	Sequence 65, Appl
35	73.4	52.4	119	4	US-09-490-324-39	Sequence 39, Appl
36	73.4	52.4	119	4	US-09-490-324-65	Sequence 65, Appl
37	73.4	52.4	139	4	US-09-471-276-837	Sequence 837, App
38	73.4	52.4	244	3	US-08-918-148-79	Sequence 79, Appl
39	73.4	52.4	244	4	US-09-138-091A-77	Sequence 77, Appl
40	73	52.1	100	4	US-09-726-219A-169	Sequence 169, App
41	72.4	51.7	140	4	US-09-471-276-850	Sequence 850, App
42	72.4	51.7	240	2	US-07-956-399-2	Sequence 2, Appli
43	72	51.4	95	3	US-09-471-276-882	Sequence 882, App
44	72	51.4	116	3	US-08-545-809A-92	Sequence 92, Appl
45	72	51.4	119	3	US-08-767-128-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-545-809A-118
; Sequence 118, Application US/0845809A
; Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

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; INFORMATION FOR SEQ ID NO: 118:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 116 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-545-809A-118

Alignment Scores:
Pred. No.:                    0.000397        Length:              116
Score:                        92.40           Matches:             19
Percent Similarity:           74.07%          Conservative:        1
Best Local Similarity:        70.37%          Mismatches:          1
Query Match:                  66.00%          Indels:              6
DB:                           3               Gaps:                0

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Db   69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  87

Qy   61 GATATTAGC 69
          |||||
Db   88 ---IleSer 89

RESULT 2
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
;   APPLICANT: EDELMAN, LENA
;   APPLICANT: MARGARITTE, CHRISTEL
;   APPLICANT: KACZOREK, MICHEL
;   APPLICANT: CHAABIHI, HASSAN
;   TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;   TITLE OF INVENTION:
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;     ADDRESSEE: P.C.
;     STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;     CITY: ARLINGTON
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22202
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/793,450
;     FILING DATE: 03-MAR-1997
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: FR 94/10566
;     FILING DATE: 02-SEP-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: OBLON, NORMAN F.
;     REGISTRATION NUMBER: 24,618
;     REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-413-3000
;     TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 123 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-793-450-4
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Alignment Scores:
Pred. No.:                    0.000405        Length:              123
Score:                        92.40           Matches:             19
Percent Similarity:           74.07%          Conservative:        1
Best Local Similarity:        70.37%          Mismatches:          1
Query Match:                  66.00%          Indels:              6
DB:                           3               Gaps:                0

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Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 3
US-09-203-768A-2
; Sequence 2, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
;   APPLICANT: Huse, William D.
;   APPLICANT: Watkins, Jeffry D.
;   TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
;   TITLE OF INVENTION: of Use
;   FILE REFERENCE: P-IX 2947
;   CURRENT APPLICATION NUMBER: US/09/203,768A
;   CURRENT FILING DATE: 1998-12-02
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-203-768A-2

Alignment Scores:
Pred. No.:                    0.000423        Length:              139
Score:                        92.40           Matches:             19
Percent Similarity:           74.07%          Conservative:        1
Best Local Similarity:        70.37%          Mismatches:          1
Query Match:                  66.00%          Indels:              6
DB:                           4               Gaps:                0

DELETED1  (1-81) x US-09-203-768A-2  (1-139)

Qy    1 GAAATCAATCATATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG  60
          ||||||||||||||||||||||||||||||||||||||||||||||    :::
Db   69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  87

Qy   61 GATATTAGC 69
          |||||
Db   88 ---IleSer 89

RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
;   APPLICANT: EDELMAN, LENA
;   APPLICANT: MARGARITTE, CHRISTEL
;   APPLICANT: KACZOREK, MICHEL
;   APPLICANT: CHAABIHI, HASSAN
;   TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;   TITLE OF INVENTION:
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;     ADDRESSEE: P.C.
;     STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;     CITY: ARLINGTON
```

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;       STATE: VA
;       COUNTRY: USA
;       ZIP: 22202
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/793,450
;       FILING DATE: 03-MAR-1997
;       CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: FR 94/10566
;       FILING DATE: 02-SEP-1994
;   ATTORNEY/AGENT INFORMATION:
;       NAME: OBLON, NORMAN F.
;       REGISTRATION NUMBER: 24,618
;       REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 703-413-3000
;       TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 472 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-793-450-8

Alignment Scores:
Pred. No.:              0.000659          Length:         472
Score:                  92.40             Matches:        19
Percent Similarity:     74.07%            Conservative:    1
Best Local Similarity:  70.37%            Mismatches:      1
Query Match:            66.00%            Indels:          6
DB:                                       Gaps:            0

DELETED1 (1-81) x US-08-793-450-8 (1-472)

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Db   69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy   61 GATATTAGC 69
         |||||
Db   88 ---IleSer 89

RESULT 5
US-09-372-425A-6
; Sequence 6, Application US/09372425A
; Patent No. 6475749
; GENERAL INFORMATION:
;   APPLICANT: Sherie L. Morrison
;   APPLICANT: Ramon Montano
;   TITLE OF INVENTION: Improved Rh Antibody
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
;       STREET: 2029 Century Park East, Suite 3800
;       CITY: Los Angeles
;       STATE: CA
;       COUNTRY: USA
;       ZIP: 90067
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy Disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: Windows 98
;       SOFTWARE: MS Word
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/372,425A
;       FILING DATE: August 11, 1999
;       CLASSIFICATION: 435
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;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Oldenakmp,David J.
;       REGISTRATION NUMBER: 29,421
;       REFERENCE/DOCKET NUMBER: 510015-223
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (310) 788-5000
;       TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO:  6:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 429 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   MOLECULE TYPE: Heavy chain without Tailpiece - AA
US-09-372-425A-6

Alignment Scores:
Pred. No.:              0.00305           Length:         429
Score:                  87.40             Matches:        18
Percent Similarity:     74.07%            Conservative:    2
Best Local Similarity:  66.67%            Mismatches:      1
Query Match:            62.43%            Indels:          6
DB:                                       Gaps:            0

DELETED1 (1-81) x US-09-372-425A-6 (1-429)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
         ||||||||||::::|||||||||||||||||||||||||||||||||   ::::
Db   69 GluIleAspHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy   61 GATATTAGC 69
         |||||
Db   88 ---IleSer 89

RESULT 6
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;   APPLICANT: Pack, Peter
;   APPLICANT: Ilag, Vic
;   APPLICANT: Ge, Liming
;   APPLICANT: Moroney, Simon
;   APPLICANT: Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;       STREET: 1251 Avenue of the Americas
;       CITY: New York
;       STATE: New York
;       COUNTRY: USA
;       ZIP: 10021
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/025,769B
;       FILING DATE: 18-FEB-1998
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: EP 95 11 3021.0
;       FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;       NAME: James F. Haley, Jr., Esq.
;       REGISTRATION NUMBER: 27,794
;       REFERENCE/DOCKET NUMBER: MORPHO/5
;   TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:    (212)596-9000
;      TELEFAX:     (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 118 amino acids
;           TYPE: amino acid
;           STRANDEDNESS:
;           TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-09-025-769B-25

Alignment Scores:
Pred. No.:                         0.0049         Length:            118
Score:                             84.40          Matches:           18
Percent Similarity:                70.37%         Conservative:      1
Best Local Similarity:             66.67%         Mismatches:        2
Query Match:                       60.29%         Indels:            6
DB:                                3              Gaps:              0

DELETED1 (1-81) x US-09-025-769B-25 (1-118)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGTCGGGCGAGTCAG  60
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Db   50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy   61 GATATTAGC  69
        ||||||
Db   69 ---IleSer  70

RESULT 7
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
;    APPLICANT: Knappik, Achim
;               Pack, Peter
;               Ilag, Vic
;               Ge, Liming
;               Moroney, Simon
;               Plueckthun, Andreas
;    TITLE OF INVENTION: Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES: 373
;    CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                    White & McAuliffe
;         STREET: 1666 K Street, N.W., Suite 300
;         CITY: Washington
;         STATE: D.C.
;         COUNTRY: USA
;         ZIP: 20006
;    COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/490,070A
;         FILING DATE: 24-Jan-2000
;    PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: EP 95 11 3021.0
;         FILING DATE: 18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;         NAME: Colin G. Sandercock, Esq.
;         REGISTRATION NUMBER: 31,298
;         REFERENCE/DOCKET NUMBER: 37629-0005
;    TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (202) 912-2000
;         TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 118 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
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;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Alignment Scores:
Pred. No.:                         0.0049         Length:            118
Score:                             84.40          Matches:           18
Percent Similarity:                70.37%         Conservative:      1
Best Local Similarity:             66.67%         Mismatches:        2
Query Match:                       60.29%         Indels:            6
DB:                                4              Gaps:              0

DELETED1 (1-81) x US-09-490-070A-25 (1-118)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGTCGGGCGAGTCAG  60
        ||||||    |||||||||||||||||||||||||||||||||||||
Db   50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy   61 GATATTAGC  69
        ||||||
Db   69 ---IleSer  70

RESULT 8
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
;    APPLICANT: Knappik, Achim
;               Pack, Peter
;               Ilag, Vic
;               Ge, Liming
;               Moroney, Simon
;               Plueckthun, Andreas
;    TITLE OF INVENTION: Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES: 373
;    CORRESPONDENCE ADDRESS:
;         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;         STREET: 1251 Avenue of the Americas
;         CITY: New York
;         STATE: New York
;         COUNTRY: USA
;         ZIP: 10021
;    COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/490,153
;         FILING DATE: 24-Jan-2000
;    PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US/09/025,769B
;         FILING DATE: 18-FEB-1998
;         APPLICATION NUMBER: EP 95 11 3021.0
;         FILING DATE: 18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;         NAME: James F. Haley, Jr., Esq.
;         REGISTRATION NUMBER: 27,794
;         REFERENCE/DOCKET NUMBER: MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (212)596-9000
;         TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 118 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
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Left column

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Alignment Scores:
Pred. No.:            0.0049        Length:         118
Score:               84.40         Matches:        18
Percent Similarity:  70.37%        Conservative:   1
Best Local Similarity: 66.67%      Mismatches:     2
Query Match:         60.29%        Indels:         6
DB:                  4             Gaps:           0

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Qy   61 GATATTAGC  69
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Db   69 ---IleSer  70

RESULT 9
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Alignment Scores:
Pred. No.:            0.0049        Length:         118
Score:               84.40         Matches:        18
Percent Similarity:  70.37%        Conservative:   1
Best Local Similarity: 66.67%      Mismatches:     2
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Query Match:         60.29%        Indels:         6
DB:                  4             Gaps:           0

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Db   50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy   61 GATATTAGC  69
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Db   69 ---IleSer  70

RESULT 10
US-08-545-809A-137
; Sequence 137, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-137

Alignment Scores:
Pred. No.:            0.0143        Length:         120
Score:               81.00         Matches:        15
Percent Similarity:  79.17%        Conservative:   4
Best Local Similarity: 62.50%      Mismatches:     5
Query Match:         57.86%        Indels:         0
DB:                  3             Gaps:           0

DELETED1 (1-81) x US-08-545-809A-137 (1-120)

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        ||||||   :::|||||||||||||||||||||||||||||||||||     :::
Db   69 GluIleHisSerGlySerThrTyrTyrAsnProSerLeuLysSerArgIleThrMet  88

Qy   61 GATATTAGCAGC  72
        :::  :::
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Db   89 SerValAspThr 92

RESULT 11
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Immunoglobulin Variants
;   NUMBER OF SEQUENCES: 65
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/466,151
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/466163
;   FILING DATE: 06-Jun-1995
;   APPLICATION NUMBER: 08/405617
;   FILING DATE: 15-MAR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/185899
;   FILING DATE: 26-JAN-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/879495
;   FILING DATE: 07-MAY-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/744768
;   FILING DATE: 14-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Svoboda, Craig G.
;   REGISTRATION NUMBER: 39,044
;   REFERENCE/DOCKET NUMBER: P0718P2C1D1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-1489
;   TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 130 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.:   0.0162   Length: 130
Score: 80.70   Matches: 18
Percent Similarity: 47.92%   Conservative: 5
Best Local Similarity: 37.50%   Mismatches: 2
Query Match: 57.64%   Indels: 23
DB: 3   Gaps: 2

DELETED1 (1-81) x US-08-466-151-5 (1-130)

Qy   4 ATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCTCAAGAGTCGGGCGAGT------ 57
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Db   52 IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy   58 CAGGATATTAGC---------- 69
         ::|||| |||
Db   72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy   70 -----------------AGCTGGTTA 78
                          :::||||:::
Db   92 AlaThrTyrTyrCysAlaTrpVal 99

RESULT 12
US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Immunoglobulin Variants
;   FILE REFERENCE: P0718P2C1D1
;   CURRENT APPLICATION NUMBER: US/08/466,163B
;   CURRENT FILING DATE: 1995-06-06
;   PRIOR APPLICATION NUMBER: US 08/405,617
;   PRIOR FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: US 08/185,899
;   PRIOR FILING DATE: 1994-01-26
;   PRIOR APPLICATION NUMBER: US 07/879,495
;   PRIOR FILING DATE: 1992-05-07
;   PRIOR APPLICATION NUMBER: US 07/744,768
;   PRIOR FILING DATE: 1991-08-14
;   NUMBER OF SEQ ID NOS: 64
;   SEQ ID NO 5
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.:   0.0162   Length: 130
Score: 80.70   Matches: 18
Percent Similarity: 47.92%   Conservative: 5
Best Local Similarity: 37.50%   Mismatches: 2
Query Match: 57.64%   Indels: 23
DB: 3   Gaps: 2

DELETED1 (1-81) x US-08-466-163B-5 (1-130)

Qy   4 ATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCTCAAGAGTCGGGCGAGT------ 57
         ||||||||||||||||||:::||||:|||||||||||||||||||||||||
Db   52 IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy   58 CAGGATATTAGC--------- 69
         ::|||| |||
Db   72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy   70 ------------------AGCTGGTTA 78
                          :::||||:::
Db   92 AlaThrTyrTyrCysAlaTrpVal 99

RESULT 13
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended
;   FILE REFERENCE: P0718P2C3US
;   CURRENT APPLICATION NUMBER: US/09/802,096
;   CURRENT FILING DATE: 2001-03-08
;   PRIOR APPLICATION NUMBER: US 08/405,617
;   PRIOR FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: US 08/185,899
;   PRIOR FILING DATE: 1994-01-26
;   PRIOR APPLICATION NUMBER: PCT/US92/06860
;   PRIOR FILING DATE: 1992-08-14
;   PRIOR APPLICATION NUMBER: US 07/879,495
;   PRIOR FILING DATE: 1992-05-07
;   PRIOR APPLICATION NUMBER: US 07/744,768
;   PRIOR FILING DATE: 1991-08-14

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; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-5

Alignment Scores:
Pred. No.:              0.0162        Length:         130
Score:                  80.70         Matches:        18
Percent Similarity:     47.92%        Conservative:   5
Best Local Similarity:  37.50%        Mismatches:     2
Query Match:            57.64%        Indels:         23
DB:                     4             Gaps:           2

DELETED1 (1-81) x US-09-802-096-5 (1-130)

Qy    4  ATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGT------  57
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Db   52  IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy   58  CAGGATATTAGC------------------  69
            :::|||  |||
Db   72  ArgAspThrSerLysAsnGlnPheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy   70  ------------AGCTGGTTA 78
                     :::|||||:::
Db   92  AlaThrTyrCysAlaTrpVal 99

RESULT 14
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. 669472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Alignment Scores:
Pred. No.:              0.0162        Length:         130
Score:                  80.70         Matches:        18
Percent Similarity:     47.92%        Conservative:   5
Best Local Similarity:  37.50%        Mismatches:     2
Query Match:            57.64%        Indels:         23
DB:                     4             Gaps:           2

DELETED1 (1-81) x US-09-802-077-5 (1-130)

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Db   52  IleAsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71

Qy   58  CAGGATATTAGC  69
            :::|||  |||
Db   72  ArgAspThrSerLysAsnGlnPheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy   70  ------------AGCTGGTTA 78
                     :::|||||:::
Db   92  AlaThrTyrCysAlaTrpVal 99

RESULT 15
US-09-471-276-835
; Sequence 835, Application US/09471276
; Patent No. 682072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 682072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 835
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -26..-1
US-09-471-276-835

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Pred. No.:              0.0254        Length:         147
Score:                  79.40         Matches:        16
Percent Similarity:     66.67%        Conservative:   2
Best Local Similarity:  59.26%        Mismatches:     3
Query Match:            56.71%        Indels:         6
DB:                     4             Gaps:           0

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Db   77  GluIleAspHisGlyGlyAsnThrAsnThrAsnProSerLeuLysSerArgVal***--- 95

Qy   61  GATATTAGC 69
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Db   96  ---IleSer 97

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score: 140
Sequence: 1 GAAATCAATCATCAGTGGAAG........ATATTAGCAGCTGGTTAGCC 81

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                 Maximum Match 100%
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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        12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	113.1	80.8	249	15	US-10-293-418-1321	Sequence 1321, Ap
3	96.4	68.9	115	17	US-10-898-408-12	Sequence 12, Appl
4	93.8	67.0	250	10	US-09-880-748-993	Sequence 993, App
5	93.8	67.0	250	15	US-10-293-418-993	Sequence 993, Appl
6	93.8	67.0	253	10	US-09-880-748-954	Sequence 954, App
7	93.8	67.0	253	15	US-10-293-418-954	Sequence 954, App
8	92.4	66.0	80	14	US-10-078-958-2	Sequence 2, Appli
9	92.4	66.0	97	14	US-10-194-975-40	Sequence 40, Appl
10	92.4	66.0	97	15	US-10-308-817-83	Sequence 83, Appl
11	92.4	66.0	97	15	US-10-032-037B-87	Sequence 87, Appl
12	92.4	66.0	97	15	US-10-029-988B-87	Sequence 87, Appl
13	92.4	66.0	97	15	US-10-033-423A-87	Sequence 87, Appl
14	92.4	66.0	97	15	US-10-453-698-83	Sequence 83, Appl
15	92.4	66.0	97	15	US-10-029-926B-87	Sequence 87, Appl
16	92.4	66.0	97	16	US-10-379-392-47	Sequence 47, Appl
17	92.4	66.0	114	17	US-10-733-532-128	Sequence 128, App
18	92.4	66.0	117	9	US-09-864-761-44315	Sequence 44315, A
19	92.4	66.0	118	15	US-10-371-942-90	Sequence 90, Appl
20	92.4	66.0	118	17	US-10-893-576-192	Sequence 192, App
21	92.4	66.0	122	15	US-10-360-828-63	Sequence 63, Appl
22	92.4	66.0	125	15	US-10-371-942-110	Sequence 110, App
23	92.4	66.0	125	15	US-10-371-942-118	Sequence 118, App
24	92.4	66.0	139	14	US-10-300-675-2	Sequence 2, Appli
25	92.4	66.0	139	17	US-10-910-124-2	Sequence 2, Appli
26	92.4	66.0	139	17	US-10-893-576-43	Sequence 43, Appli
27	92.4	66.0	142	17	US-10-484-790A-10	Sequence 10, Appl
28	92.4	66.0	223	10	US-09-972-656-66	Sequence 66, Appl
29	92.4	66.0	229	10	US-09-972-656-82	Sequence 82, Appl
30	92.4	66.0	230	10	US-09-972-656-72	Sequence 72, Appl
31	92.4	66.0	249	10	US-09-880-748-957	Sequence 957, App
32	92.4	66.0	249	15	US-10-293-418-957	Sequence 957, App
33	92.4	66.0	250	10	US-09-880-748-1413	Sequence 1413, Ap
34	92.4	66.0	250	15	US-10-293-418-1413	Sequence 1413, Ap
35	92.4	66.0	253	10	US-09-880-748-1333	Sequence 1333, Ap
36	92.4	66.0	253	15	US-10-293-418-1333	Sequence 1333, Ap
37	92.4	66.0	254	10	US-09-880-748-1659	Sequence 1659, Ap
38	92.4	66.0	254	15	US-10-293-418-1659	Sequence 1659, Ap
39	92.4	66.0	450	17	US-10-484-790A-17	Sequence 17, Appl
40	92.4	66.0	453	17	US-10-484-790A-18	Sequence 18, Appl
41	90.4	64.6	246	10	US-09-880-748-1847	Sequence 1847, Ap
42	90.4	64.6	246	15	US-10-293-418-1847	Sequence 1847, Ap
43	90.3	64.5	123	14	US-10-269-805-31	Sequence 31, Appl
44	90.3	64.5	123	14	US-10-269-805-55	Sequence 55, Appl
45	88.4	63.1	255	10	US-09-880-748-1642	Sequence 1642, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben et al.
;   TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;   FILE REFERENCE: PF523
;   CURRENT APPLICATION NUMBER: US/09/880,748
;   CURRENT FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/212,210
;   PRIOR FILING DATE: 2000-06-15
;   PRIOR APPLICATION NUMBER: 60/240,816
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE: 2000-10-17
;   PRIOR APPLICATION NUMBER: 60/276,248
;   PRIOR FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/293,499
;   PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.:   2.81e-05   Length: 249
Score: 113.10   Matches: 26
Percent Similarity: 20.63%   Conservative: 0
Best Local Similarity: 20.63%   Mismatches: 1
Query Match: 80.79%   Indels: 99
DB: Gaps: 1

DELETED1 (1-81) x US-09-880-748-1321 (1-249)

```
Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAAGAGT----------- 48
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 ------------------------------------------------------------ 48

Db   70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89

Qy   48 ------------------------------------------------------------ 48

Db   90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109

Qy   48 ------------------------------------------------------------ 48

Db  110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerGlyGlyGlyGly 129

Qy   48 ------------------------------------------------------------ 48

Db  130 GlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGlnSerPro 149

Qy   49 ---------------------------------------CGGGCGGAGTCAGGAT 63
                                               |||||||||
Db  150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169

Qy   64 ATTAGCAGCTGGTTAGCC 81
          |||||||||
Db  170 IleSerSerTrpLeuAla 175
```

RESULT 2
US-10-293-418-1321
; Sequence 1321, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1321

Alignment Scores:
Pred. No.:   2.81e-05   Length: 249
Score: 113.10   Matches: 26
Percent Similarity: 20.63%   Conservative: 0
Best Local Similarity: 20.63%   Mismatches: 1
Query Match: 80.79%   Indels: 99
DB: Gaps: 1

DELETED1 (1-81) x US-10-293-418-1321 (1-249)

```
Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAAGAGT----------- 48
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69

Qy   48 ------------------------------------------------------------ 48

Db   70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89

Qy   48 ------------------------------------------------------------ 48

Db   90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109

Qy   48 ------------------------------------------------------------ 48

Db  110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerGlyGlyGlyGly 129

Qy   48 ------------------------------------------------------------ 48

Db  130 GlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGlnSerPro 149

Qy   49 ---------------------------------------CGGGCGGAGTCAGGAT 63
                                               |||||||||
Db  150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169

Qy   64 ATTAGCAGCTGGTTAGCC 81
          |||||||||
Db  170 IleSerSerTrpLeuAla 175
```

RESULT 3
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: GALIBERT, Laurent J.
; APPLICANT: YAN, Wei
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.:   0.00314   Length: 115
Score: 96.40   Matches: 19
Percent Similarity: 41.18%   Conservative: 2
Best Local Similarity: 37.25%   Mismatches: 4
Query Match: 68.86%   Indels: 26
DB: 17   1

```
DELETED1 (1-81) x US-10-898-408-12 (1-115)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||    :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMet 69

Qy   61 GATATTAGC------------------- 69
        :::
Db   70 SerValAspThrSerLysGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAsp 89

Qy   70 -------------------AGCTGG 75
                           |||||
Db   90 ThrAlaValTyrTyrCysAlaArgValSerTrp 100
```

RESULT 4
US-09-880-748-993
; Sequence 993, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-993

```
Alignment Scores:
Pred. No.:              0.00772        Length:          250
Score:                  93.80          Matches:          20
Percent Similarity:     80.77%         Conservative:      1
Best Local Similarity:  76.92%         Mismatches:        3
Query Match:            67.00%         Indels:            2
DB:                     10             Gaps:              1

DELETED1 (1-81) x US-09-880-748-993 (1-250)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
        ||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75
```

RESULT 5
US-10-293-418-993
; Sequence 993, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-993

```
Alignment Scores:
Pred. No.:              0.00772        Length:          250
Score:                  93.80          Matches:          20
Percent Similarity:     80.77%         Conservative:      1
Best Local Similarity:  76.92%         Mismatches:        3
Query Match:            67.00%         Indels:            2
DB:                     15             Gaps:              1

DELETED1 (1-81) x US-10-293-418-993 (1-250)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG------ 54
        |||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
        ||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75
```

RESULT 6
US-09-880-748-954
; Sequence 954, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-954

```
Alignment Scores:
Pred. No.:              0.00774        Length:          253
Score:                  93.80          Matches:          20
Percent Similarity:     80.77%         Conservative:      1
Best Local Similarity:  76.92%         Mismatches:        3
Query Match:            67.00%         Indels:            2
DB:                     10             Gaps:              1
```

; TITLE OF INVENTION: PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2

Alignment Scores:
Pred. No.:   0.0094   Length: 80
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 14   Gaps: 0

DELETED1 (1-81) x US-10-078-958-2 (1-80)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCAAGAGTCGGGCGAGTCAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   33 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 51

Qy   61 GATATTAGC 69
           |||||
Db   52 ---IleSer 53

RESULT 9
US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40

Alignment Scores:
Pred. No.:   0.00974   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: 14   Gaps: 0

DELETED1 (1-81) x US-10-194-975-40 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCAAGAGTCGGGCGAGTCAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
           |||||
Db   69 ---IleSer 70

RESULT 10
US-10-308-817-83

DELETED1 (1-81) x US-09-880-748-954 (1-253)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG------ 54
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
           ||||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75

RESULT 7
US-10-293-418-954
; Sequence 954, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-954

Alignment Scores:
Pred. No.:   0.00774   Length: 253
Score: 93.80   Matches: 20
Percent Similarity: 80.77%   Conservative: 1
Best Local Similarity: 76.92%   Mismatches: 3
Query Match: 67.00%   Indels: 2
DB: 15   Gaps: 1

DELETED1 (1-81) x US-10-293-418-954 (1-253)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCG------ 54
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy   55 AGTCAGGATATTAGCAGC 72
           ||||||||| |||:::
Db   70 SerGlnAspThrSerAsn 75

RESULT 8
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING

```
; Sequence 83, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
;   APPLICANT: Rother, Russell
;   APPLICANT: Wu, Dayang
;   TITLE OF INVENTION: HYBRID ANTIBODIES
;   FILE REFERENCE: 1087-37
;   CURRENT APPLICATION NUMBER: US/10/308,817
;   CURRENT FILING DATE: 2002-12-03
;   NUMBER OF SEQ ID NOS: 195
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: human
US-10-308-817-83

Alignment Scores:
Pred. No.:                 0.00974
Score:                     92.40
Percent Similarity:        74.07%
Best Local Similarity:     70.37%
Query Match:               66.00%
DB:                        15

          Length:        97
          Matches:       19
          Conservative:  1
          Mismatches:    1
          Indels:        6
          Gaps:          0

DELETED1 (1-81) x US-10-308-817-83 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||          :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          ||||||
Db   69 ---IleSer 70
```

```
RESULT 11
US-10-032-037B-87
; Sequence 87, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
;   APPLICANT: Bio-Technology General Corp.
;   TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
;   TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
;   FILE REFERENCE: 10793/44
;   CURRENT APPLICATION NUMBER: US/10/032,037B
;   CURRENT FILING DATE: 2001-12-31
;   PRIOR APPLICATION NUMBER: 60/258,948
;   PRIOR FILING DATE: 2000-12-29
;   NUMBER OF SEQ ID NOS: 204
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-032-037B-87

Alignment Scores:
Pred. No.:                 0.00974
Score:                     92.40
Percent Similarity:        74.07%
Best Local Similarity:     70.37%
Query Match:               66.00%
DB:                        15

          Length:        97
          Matches:       19
          Conservative:  1
          Mismatches:    1
          Indels:        6
          Gaps:          0

DELETED1 (1-81) x US-10-032-037B-87 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||          :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          ||||||
Db   69 ---IleSer 70
```

```
RESULT 12
US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
;   APPLICANT: Bio-Technology General Corp.
;   TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
;   TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
;   FILE REFERENCE: 10793/46
;   CURRENT APPLICATION NUMBER: US/10/029,988B
;   CURRENT FILING DATE: 2001-12-31
;   PRIOR APPLICATION NUMBER: 60/258,948
;   PRIOR FILING DATE: 2000-12-29
;   NUMBER OF SEQ ID NOS: 204
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-029-988B-87

Alignment Scores:
Pred. No.:                 0.00974
Score:                     92.40
Percent Similarity:        74.07%
Best Local Similarity:     70.37%
Query Match:               66.00%
DB:                        15

          Length:        97
          Matches:       19
          Conservative:  1
          Mismatches:    1
          Indels:        6
          Gaps:          0

DELETED1 (1-81) x US-10-029-988B-87 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||          :::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          ||||||
Db   69 ---IleSer 70
```

```
RESULT 13
US-10-032-423A-87
; Sequence 87, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
;   APPLICANT: Bio-Technology General Corp.
;   TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
;   TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
;   FILE REFERENCE: 10793/45
;   CURRENT APPLICATION NUMBER: US/10/032,423A
;   CURRENT FILING DATE: 2001-12-31
;   PRIOR APPLICATION NUMBER: US/10/032,423A
;   PRIOR FILING DATE: 12/29/2000
;   NUMBER OF SEQ ID NOS: 204
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.:                 0.00974
Score:                     92.40
Percent Similarity:        74.07%
Best Local Similarity:     70.37%
Query Match:               66.00%
DB:                        15

          Length:        97
          Matches:       19
          Conservative:  1
          Mismatches:    1
          Indels:        6
          Gaps:          0

DELETED1 (1-81) x US-10-032-423A-87 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||          :::
```

```
Db        50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db        50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy        61 GATATTAGC 69                      Qy        61 GATATTAGC 69
              |||||                                        |||||
Db        69 ---IleSer 70                      Db        69 ---IleSer 70


RESULT 14
US-10-453-698-83
; Sequence 83, Application US/10453698
; Publication No. US2004038308A1
; GENERAL INFORMATION:
;   APPLICANT: Rother, Russell
;   TITLE OF INVENTION: HYBRID ANTIBODIES
;   FILE REFERENCE: 82 CIP (1087-37 CIP)
;   CURRENT APPLICATION NUMBER: US/10/453,698
;   CURRENT FILING DATE: 2003-06-03
;   NUMBER OF SEQ ID NOS: 196
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: human
US-10-453-698-83

Alignment Scores:
Pred. No.:                              Length:         97
Score:                    0.00974       Matches:        19
Percent Similarity:       92.40         Conservative:   1
Best Local Similarity:    74.07%        Mismatches:     1
Query Match:              70.37%        Indels:         6
DB:                       66.00%        Gaps:           0
                          15
US-10-453-698-83

DELETED1 (1-81) x US-10-453-698-83 (1-97)

Qy         1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGTCGGGGCGAGTCAG 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db        50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy        61 GATATTAGC 69
              |||||
Db        69 ---IleSer 70


RESULT 15
US-10-029-926B-87
; Sequence 87, Application US/10029926B
; Publication No. US2004007301lA1
; GENERAL INFORMATION:
;   APPLICANT: HAGAY, et al.
;   TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
;   FILE REFERENCE: 10793/50
;   CURRENT APPLICATION NUMBER: US/10/029,926B
;   CURRENT FILING DATE: 2001-12-31
;   PRIOR APPLICATION NUMBER: 60/258,948
;   PRIOR FILING DATE: 12/29/2000
;   NUMBER OF SEQ ID NOS: 203
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-029-926B-87

Alignment Scores:
Pred. No.:                              Length:         97
Score:                    0.00974       Matches:        19
Percent Similarity:       92.40         Conservative:   1
Best Local Similarity:    74.07%        Mismatches:     1
Query Match:              70.37%        Indels:         6
DB:                       66.00%        Gaps:           0
                          15
US-10-029-926B-87

DELETED1 (1-81) x US-10-029-926B-87 (1-97)

Qy         1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGTCGGGGCGAGTCAG 60
```

Search completed: August 4, 2005, 19:56:40
Job time : 107 secs

OM nucleic - protein search, using frame_plus_n2p model

Copyright   GenCore version 5.1.6   (c) 1993 - 2005   Compugen Ltd.

Run on: August 4, 2005, 19:22:55 ; Search time 26 Seconds
(without alignments)
599.504 Million cell updates/sec

Title: DELETED1
Perfect score: 140
Sequence: 1 GAAATCAATCATAGTGGAAG.........ATATTAGCAGCTGGTTAGCC 81

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext   0.1
Ygapop 10.0 , Ygapext   0.1
Fgapop 6.0 , Fgapext   0.1
Delop   6.0 , Delext   0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3A/runat_04082005_120125_18808/app_query.fasta_1.263
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3A @CGN_1_1_63 @runat_04082005_120125_18808 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :   PIR_79:*
1:   pir1:*
2:   pir2:*
3:   pir3:*
4:   pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	67.1	97	2	S26806	Ig heavy chain V r
2	93.9	67.1	140	2	S78052	Ig heavy chain pre
3	92.4	66.0	97	2	S26898	Ig heavy chain V r
4	92.4	66.0	97	2	S26805	Ig heavy chain V r
5	92.4	66.0	106	2	S37454	Ig mu chain - huma
6	92.4	66.0	122	2	JL0047	Ig heavy chain V r
7	92.4	66.0	126	2	S47010	Ig heavy chain V4.
8	92.4	66.0	133	2	PS0341	Ig heavy chain V-D
9	92.4	66.0	140	2	A49045	Ig heavy chain V r
10	92.4	66.0	143	2	B49028	Ig heavy chain V-I
11	92.4	66.0	231	2	B23746	Ig Fab region IV-J
12	88.4	63.1	97	2	G34964	Ig heavy chain V-I
13	84.4	60.3	98	2	S26905	Ig heavy chain V r
14	83.1	59.6	97	2	S14474	Ig heavy chain V r
15	81.4	58.1	129	2	S44114	Ig heavy chain V r
16	80	57.4	134	2	S54906	Ig heavy chain V r
17	79.1	57.1	123	2	S30529	Ig heavy chain V r
18	78.4	56.5	140	2	I37782	Ig variable region
19	78.4	56.0	98	2	S26904	Ig heavy chain V r
20	78.4	56.0	145	2	S78055	Ig heavy chain pre
21	77.4	56.0	146	1	G1HUH2	Ig heavy chain pre
22	77.4	55.3	114	2	I72667	cold agglutinin FS
23	77.3	55.2	130	2	S31673	Ig heavy chain pre
24	77	55.0	134	2	B24672	Ig heavy chain pre
25	75.4	53.9	97	2	JH0428	Ig gamma chain V r
26	74.4	53.1	106	2	S26464	Ig heavy chain V r
27	74	52.9	116	2	S38718	Ig heavy chain V r
28	73.4	52.4	97	2	S26906	Ig heavy chain V r
29	73.4	52.4	97	2	S12416	Ig heavy chain V r
30	73.4	52.4	99	2	S12412	Ig heavy chain V r
31	73.4	52.4	105	2	S44125	Ig lambda chain V
32	73.4	52.4	116	2	B26340	Ig heavy chain pre
33	73.4	52.4	118	2	A26340	Ig heavy chain pre
34	73.4	52.2	130	2	S31690	Ig heavy chain V r
35	73.1	52.2	127	2	S19668	Ig heavy chain V r
36	72	51.4	97	2	S26804	Ig heavy chain V r
37	72	51.4	97	2	S26808	Ig heavy chain V r
38	72	51.4	116	2	S18557	Ig heavy chain V r
39	72	51.4	137	2	S31676	Ig heavy chain V r
40	72	51.4	139	2	S31696	Ig heavy chain V r
41	72	51.4	139	2	S31586	Ig heavy chain V r
42	71.5	51.1	109	2	PH1673	Ig heavy chain V r
43	71.4	51.0	97	2	PL0118	Ig heavy chain V-I
44	71.4	51.0	98	2	S26902	Ig heavy chain V r
45	71.4	51.0	98	2	S12421	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S26806
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26806
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26806; MUID:92201299; PMID:1348029
A;Accession: S26806
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000731   Length: 97
Score: 94.00   Matches: 17
Percent Similarity: 83.33%   Conservative: 3
Best Local Similarity: 70.83%   Mismatches: 4
Query Match: 67.14%   Indels: 0
DB: 2   Gaps: 0

DELETED1 (1-81) x S26806 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCCAAGAGTCGGGCGGGAGTCAG 60
                                                          ::::
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgIleThrMet 69

Qy   61 GATATTAGCAGC 72
           :::   :::
Db   70 SerValAspThr 73

RESULT 2

S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
R;Harindranath, N.
A;Accession: S78052; S23717
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000771   Length: 140
Score: 93.90   Matches: 21
Percent Similarity: 33.85%   Conservative: 1
Best Local Similarity: 32.31%   Mismatches: 2
Query Match: 67.07%   Indels: 41
DB: Gaps: 1

DELETED1 (1-81) x S78052 (1-140)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||| ::|
Db   64 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 82

Qy   61 GATATTAGC------------------------------------- 69
          |||||
Db   83 ---IleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAla 101

Qy   70 --AGCTGG 75
                                                    |||
Db 102 AlaAspThrAlaValTyrTyrCysAlaArgGlyGlySerValLeuArgPheLeuGluTrp 121

Qy   76 TTA 78
          |||
Db 122 Leu 122

RESULT 3
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
A;Experimental source: clone DP-63
A;Accession: S26898; S12420
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26898
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12420

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <SAN>
A;Cross-references: EMBL:X56364
A;Experimental source: V(H)4.2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00119   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: Gaps: 0

DELETED1 (1-81) x S26898 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||| ::|
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 4
S26805
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.00119   Length: 97
Score: 92.40   Matches: 19
Percent Similarity: 74.07%   Conservative: 1
Best Local Similarity: 70.37%   Mismatches: 1
Query Match: 66.00%   Indels: 6
DB: Gaps: 0

DELETED1 (1-81) x S26805 (1-97)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||| ::|
Db   50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70

RESULT 5
S37454
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from

A;Reference number: S37453
A;Accession: S37454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>
A;Cross-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

```
Alignment Scores:
Pred. No.:              0.0012      Length:         106
Score:                  92.40       Matches:        19
Percent Similarity:     74.07%      Conservative:   1
Best Local Similarity:  70.37%      Mismatches:     1
Query Match:            66.00%      Indels:         6
DB:                     2           Gaps:           0

DELETED1 (1-81) x S37454 (1-106)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db  28 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 46

Qy  61 GATATTAGC 69
        |||||
Db  47 ---IleSer 48
```

RESULT 6
JL0047
Ig heavy chain V region precursor (clone cR18) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: JL0047
R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5
A;Reference number: JL0047; MUID:88258392; PMID:3133445
A;Accession: JL0047
A;Molecule type: mRNA
A;Residues: 1-122 <BAE>
A;Experimental source: T-cell line RPMI 8402
A;Note: the authors translated the reading frame which extends to the stop codon; the se
A;Note: this sequence belongs to the VH II subgroup
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-105/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:              0.00121     Length:         122
Score:                  92.40       Matches:        19
Percent Similarity:     74.07%      Conservative:   1
Best Local Similarity:  70.37%      Mismatches:     1
Query Match:            66.00%      Indels:         6
DB:                     2           Gaps:           0

DELETED1 (1-81) x JL0047 (1-122)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db  58 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 76

Qy  61 GATATTAGC 69
        |||||
Db  77 ---IleSer 78
```

RESULT 7
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S47010
R;Mahmoudi, M.; Gabyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bir
A;Reference number: S47009
A;Accession: S47010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:              0.00121     Length:         126
Score:                  92.40       Matches:        19
Percent Similarity:     74.07%      Conservative:   1
Best Local Similarity:  70.37%      Mismatches:     1
Query Match:            66.00%      Indels:         6
DB:                     2           Gaps:           0

DELETED1 (1-81) x S47010 (1-126)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db  50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy  61 GATATTAGC 69
        |||||
Db  69 ---IleSer 70
```

RESULT 8
PS0341
Ig heavy chain V-D-J region (RAMOS) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C;Accession: PS0341
R;Ratech, H.
Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
A;Reference number: PS0341; MUID:92171937; PMID:1540170
A;Accession: PS0341
A;Molecule type: mRNA
A;Residues: 1-133 <RAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-38/Region: framework 1
F;39-43/Region: complementarity-determining 1
F;44-57/Region: framework 2
F;58-74/Region: complementarity-determining 2
F;75-106/Region: framework 3

```
Alignment Scores:
Pred. No.:              0.00121     Length:         133
Score:                  92.40       Matches:        19
Percent Similarity:     74.07%      Conservative:   1
Best Local Similarity:  70.37%      Mismatches:     1
Query Match:            66.00%      Indels:         6
DB:                     2           Gaps:           0

DELETED1 (1-81) x PS0341 (1-133)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db  58 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 76

Qy  61 GATATTAGC 69
        |||||
Db  77 ---IleSer 78
```

RESULT 9
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <GRI>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                    0.00122          Length:            140
Percent Similarity:       92.40            Matches:            19
Best Local Similarity:    74.07%           Conservative:        1
Query Match:              70.37%           Mismatches:          1
DB:                       66.00%           Indels:              6
                          2                Gaps:                0

DELETED1 (1-81) x A49045 (1-140)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   69 GluIleAsnHisSerGlyThrThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy   61 GATATTAGC 69
          |||||
Db   88 ---IleSer 89
```

RESULT 10
B49028
Ig heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: B49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-143 <TIM>
A;Cross-references: GB:S64473; NID:g236906; PIDN:AAB20012.1; PID:g236907
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                    0.00122          Length:            143
Percent Similarity:       92.40            Matches:            19
Best Local Similarity:    74.07%           Conservative:        1
Query Match:              70.37%           Mismatches:          1
DB:                       66.00%           Indels:              6
                          2                Gaps:                0

DELETED1 (1-81) x B49028 (1-143)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   50 GluIleAsnHisSerGlyThrThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70
```

RESULT 11

B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: B23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
F;140-209/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                    0.00125          Length:            231
Percent Similarity:       92.40            Matches:            19
Best Local Similarity:    74.07%           Conservative:        1
Query Match:              70.37%           Mismatches:          1
DB:                       66.00%           Indels:              6
                          2                Gaps:                0

DELETED1 (1-81) x B23746 (1-231)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   49 GluIleAsnHisSerGlyThrThrAsnTyrAsnProSerLeuLysSerArgValThr--- 67

Qy   61 GATATTAGC 69
          |||||
Db   68 ---IleSer 69
```

RESULT 12
G34964
Ig heavy chain V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
A;Molecule type: mRNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:
Score:                    0.00404          Length:             97
Percent Similarity:       88.40            Matches:            18
Best Local Similarity:    70.37%           Conservative:        1
Query Match:              66.67%           Mismatches:          2
DB:                       63.14%           Indels:              6
                          2                Gaps:                0

DELETED1 (1-81) x G34964 (1-97)

Qy    1 GAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   50 GluIleAsnHisSerGlyGlyThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy   61 GATATTAGC 69
          |||||
Db   69 ---IleSer 70
```

RESULT 13
S26905
Ig heavy chain V region (DP-70 / 4.19) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline v(H) sequences reveals about fifty groups of v
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human v(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12419
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <SAN>
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:	0.0137	Length:	98
Score:	84.40	Matches:	18
Percent Similarity:	70.37%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	2
Query Match:	60.29%	Indels:	6
DB:	2	Gaps:	0

DELETED1 (1-81) x S26905 (1-98)

```
Qy    1  GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGTCGGGCGAGTCAG  60
            |||| |||||||||||||||||||||||||||||        |||     :||
Db   51  GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  69

Qy   61  GATATTAGC 69
            |||||
Db   70  ---IleSer 71
```

RESULT 14
S14474
Ig heavy chain v region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S14474
R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H
submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Accession: S14474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <ESJ>
A;Cross-references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:g1335354
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:	0.0186	Length:	97
Score:	83.40	Matches:	18
Percent Similarity:	70.37%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	2
Query Match:	59.57%	Indels:	6
DB:	2	Gaps:	0

DELETED1 (1-81) x S14474 (1-97)

```
Qy    1  GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGTCGGGCGAGTCAG  60
            |||| ||||||||||||||||||||||||||||||        |||     :||
Db   50  GluIleHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68

Qy   61  GATATTAGC 69
            |||||
Db   69  ---IleSer 70
```

RESULT 15
S44114
Ig heavy chain v region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAW>
A;Cross-references: EMBL:Z31579; NID:g472968; PIDN:CAA83451.1; PID:g940525
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:	0.0348	Length:	129
Score:	81.40	Matches:	17
Percent Similarity:	67.86%	Conservative:	2
Best Local Similarity:	60.71%	Mismatches:	3
Query Match:	58.14%	Indels:	6
DB:	2	Gaps:	0

DELETED1 (1-81) x S44114 (1-129)

```
Qy    1  GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAAGAGTCGGGCGAGTCAG  60
            |||| ||||||||||||||||||||||||||||||        |||     :||
Db   51  GluIleTyrHisSerGlySerThrAsnTyrAsnProSerPheLysSerArgValThr---  69

Qy   61  GATATTAGCAGC 72
            |||||| :::
Db   70  ---IleSerAla 72
```

Search completed: August 4, 2005, 19:38:53
Job time : 28 secs

```
            GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August  4, 2005, 19:04:23 ; Search time 108 Seconds
                            (without alignments)
                      768.119 Million cell updates/sec

Title:          DELETED1
Perfect score:  140
Sequence:       1 GAAATCAATCATAGTGGAAG.........ATATTAGCAGCTCGTTAGCC 81

Scoring table:  BLOSUM62
        Xgapop 10.0 , Xgapext  0.1
        Ygapop 10.0 , Ygapext  0.1
        Fgapop  6.0 , Fgapext  0.1
        Delop   6.0 , Delext   0.1

Searched:       1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:     3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3A/runat_04082005_120125_18797/app_query.fasta_1.263
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3A @CGN 1 1 244 @runat_04082005_120125_18797 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.1 -XGAPOP=10 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :     UniProt_03:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
```

Result No.	Score	% Match	Query Length	DB	ID	Description
1	92.4	66.0	116	2	Q7Z3Y6	Q7Z3Y6 homo sapien
2	92.4	66.0	595	2	Q8WUX4	Q8WUX4 homo sapien
3	92.4	66.0	597	2	Q6GMX5	Q6GMX5 homo sapien
4	92.4	66.0	597	2	Q9BU10	Q9BU10 homo sapien
5	92.4	61.7	625	2	Q96AA6	Q96AA6 homo sapien
6	86.4	60.3	597	2	Q9BQB8	Q9BQB8 homo sapien
7	84.4	58.1	576	2	Q6P4I8	Q6P4I8 homo sapien
8	81.3	56.0	477	2	Q6GMX7	Q6GMX7 homo sapien
9	78.4	52.6	146	1	HV2I_HUMAN	P06331 homo sapien
10	73.7	51.9	139	2	Q86SX2	Q86SX2 homo sapien
11	72.6	51.4	479	2	Q99M22	Q99M22 mus musculu
12	72	51.4	465	2	Q6GMX6	Q6GMX6 homo sapien
13	72	50.4	620	2	Q96EY0	Q96EY0 homo sapien
14	70.6	49.5	262	2	Q65ZI1	Q65ZI1 mus musculu
15	69.3	49.4	119	2	Q9U173	Q9U173 homo sapien
16	69.1		113	1	HV47_MOUSE	P01823 mus musculu
17	69	49.3	116	1	HV61_MOUSE	P18532 mus musculu
18	67.4	48.1	2348	2	Q8Z027	Q8Z027 anabaena sp
19	66.9	47.8	476	2	Q6GMX1	Q6GMX1 homo sapien
20	65	46.4	116	1	HV60_MOUSE	P18531 mus musculu
21	65	46.4	478	2	Q6NYH3	Q6NYH3 homo sapien
22	64	45.7	478	2	Q7Z379	Q7Z379 homo sapien
23	60.8	43.4	3118	2	O17575	O17575 caenorhabdi
24	59.4	42.4	150	2	O95973	O95973 homo sapien
25	59	42.1	136	2	Q6LBQ5	Q6LBQ5 mus musculu
26	59	42.1	137	1	HV46_MOUSE	P01822 mus musculu
27	58.7	41.9	209	2	Q8XWU0	Q8XWU0 ralstonia s
28	57.5	41.1	963	2	Q8P5M2	Q8P5M2 xanthomonas
29	57.5	41.1	1160	1	TFC3_YEAST	P34111 saccharomyc
30	57.4	41.0	496	2	Q96KX8	Q96KX8 homo sapien
31	57.1	40.8	163	2	Q84F35	Q84F35 streptomyce
32	56.7	40.5	212	2	Q926K5	Q926K5 listeria in
33	56.6	40.4	408	1	YBX0_ARATH	Q9ZQ34 arabidopsis
34	56.4	40.3	390	2	Q6HH60	Q6HH60 bacillus th
35	56.4	40.3	545	2	Q6HH58	Q6HH58 bacillus th
36	56.4	40.3	588	2	Q813F9	Q813F9 bacillus ce
37	56.3	40.2	1177	2	Q664Z3	Q664Z3 yersinia ps
38	56.3	40.2	589	2	Q82B26	Q82B26 yersinia pe
39	56	39.9	589	2	Q9K7H7	Q9K7H7 bacillus ha
40	55.9	39.9	421	2	Q88115	Q88115 pseudomonas
41	55.8	39.9	877	1	SEU_ARATH	Q8W234 arabidopsis
42	55.7	39.8	193	2	Q63FQ9	Q63FQ9 bacillus ce
43	55.7	39.8	193	2	Q73DA2	Q73DA2 bacillus ce
44	55.7	39.8	193	2	Q81HP9	Q81HP9 bacillus ce
45	55.7	39.8	193	2	Q81UW5	Q81UW5 bacillus an

```
                        ALIGNMENTS

RESULT 1
Q7Z3Y6
ID   Q7Z3Y6               PRELIMINARY;      PRT;    116 AA.
AC   Q7Z3Y6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rearranged VH4-34 V gene segment (Fragment).
GN   Name=VH4-34;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564425; CAD92032.1; -.
DR   HSSP; P18532; 1KCV.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1        1
FT   NON_TER     116      116
SQ   SEQUENCE   116 AA;  12902 MW;  CE3D8A46616C908 CRC64;

Alignment Scores:
Pred. No.:               0.00232
Score:                   92.40          Length:        116
Percent Similarity:      74.07%         Matches:        19
Best Local Similarity:   70.37%         Conservative:    1
Query Match:             66.00%         Mismatches:      1
DB:                      2              Indels:          6
                                        Gaps:            0

DELETED1 (1-81) x Q7Z3Y6 (1-116)

Qy       1 GAAATCAATCATAGTGGAAGCAGAGCACCAACTACAACCGTCTTCAAGAGTCGGGCGAGTCAG 60
```

```
Db            50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr---  68
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   :::

Qy            61 GATATTAGC 69
                 ||||||
Db            69 ---IleSer 70


RESULT 2
Q8WUX4
ID   Q8WUX4         PRELIMINARY;       PRT;   595 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019235; AAH19235.2; -.
DR   PIR; G34964; G34964.
DR   HSSP; P01861; 1ADQ.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   595 AA;   65290 MW;   0D4B50776545714E CRC64;

Alignment Scores:
Pred. No.:                  0.00292        Length:              595
Score:                      92.40          Matches:             19
Percent Similarity:         74.07%         Conservative:        1
Best Local Similarity:      70.37%         Mismatches:          1
Query Match:                66.00%         Indels:              6
DB:                         2              Gaps:                0

DELETED1 (1-81) x Q8WUX4 (1-595)

Qy             1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCAAGAGTCGGGCGAGTCAG  60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db            76 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 94
```

```
Qy            61 GATATTAGC 69
                 ||||||
Db            95 ---IleSer 96


RESULT 3
Q6GMX5
ID   Q6GMX5         PRELIMINARY;       PRT;   597 AA.
AC   Q6GMX5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073767; AAH73767.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;   65304 MW;   2A1E75F6AED85230 CRC64;

Alignment Scores:
Pred. No.:                  0.00292        Length:              597
Score:                      92.40          Matches:             19
Percent Similarity:         74.07%         Conservative:        1
Best Local Similarity:      70.37%         Mismatches:          1
Query Match:                66.00%         Indels:              6
DB:                         2              Gaps:                0

DELETED1 (1-81) x Q6GMX5 (1-597)

Qy             1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCAAGAGTCGGGCGAGTCAG 60
```

RESULT 4 / RESULT 5

```
Db              |||||||  |||||||||||||||||||||||||||||||  .::
         69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87

Qy       61 GATATTAGC 69
                |||||
Db       88 ---IleSer 89
```

RESULT 4
```
Q9BU10
ID   Q9BU10            PRELIMINARY;      PRT;   597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE  597 AA;  65274 MW;  2DAFA8FB7E055851 CRC64;

Alignment Scores:
Pred. No.:                        0.00292       Length:            597
Score:                            92.40%        Matches:           19
Percent Similarity:               74.07%        Conservative:      1
Best Local Similarity:            70.37%        Mismatches:        6
Query Match:                      66.00%        Indels:            0
DB:                               2             Gaps:              0

DELETED1 (1-81) x Q9BU10 (1-597)

Qy       1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   .::
Db      69 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
```

RESULT 5
```
Q96AA6
ID   Q96AA6            PRELIMINARY;      PRT;   625 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.2; -.
DR   PIR; S15590; S15590.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE  625 AA;  68610 MW;  F62FAB3ADE7ECBFE CRC64;

Alignment Scores:
Pred. No.:                        0.00294       Length:            625
Score:                            92.40%        Matches:           19
Percent Similarity:               74.07%        Conservative:      1
Best Local Similarity:            70.37%        Mismatches:        1
Query Match:                      66.00%        Indels:            6
DB:                               2             Gaps:              0

DELETED1 (1-81) x Q96AA6 (1-625)

Qy       1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
```

```
Db      76 GluIleAsnHisSerGlySerThrThrAsnProSerLeuLysSerArgValThr--- 94
           ||||||||||||||||||||||||||||||||||||||              .::
Qy      61 GATATTAGC 69
           |||||
Db      95 ---IleSer 96
```

```
RESULT 6
Q9BQB8
ID   Q9BQB8          PRELIMINARY;      PRT;   597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Alignment Scores:
Pred. No.:                   0.0197          Length:         597
Score:                      86.40            Matches:         18
Percent Similarity:         70.37%           Conservative:     1
Best Local Similarity:      66.67%           Mismatches:       2
Query Match:                61.71%           Indels:           6
DB:                                          Gaps:             0

DELETED1 (1-81) x Q9BQB8 (1-597)
```

```
Qy       1 GAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCCAAGAGTCGGGCGCAGTCAG 60
           |||||||||||||||||||||||||||||||||||||||||||             .:::
Db      69 GluIleAsnHisSerGlyIleThrAsnProSerLeuLysSerArgValThr--- 87
```

```
Db      61 GATATTAGC 69
           |||||
Db      88 ---IleSer 89
```

```
RESULT 7
Q6P4I8
ID   Q6P4I8          PRELIMINARY;      PRT;   576 AA.
AC   Q6P4I8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHD protein.
GN   Name=IGHD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063384; AAH63384.1; -.
DR   HSSP; P01820; 1A7N.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG1; 1.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ   SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1B CRC64;

Alignment Scores:
Pred. No.:                   0.0371          Length:         576
Score:                      84.40            Matches:         18
Percent Similarity:         70.37%           Conservative:     1
Best Local Similarity:      66.67%           Mismatches:       2
Query Match:                60.29%           Indels:           6
DB:                                          Gaps:             0

DELETED1 (1-81) x Q6P4I8 (1-576)
```

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db   77 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 95

Qy   61 GATATTAGC 69
          |||||
Db   96 ---IleSer 97

RESULT 8
Q6GMX7
ID   Q6GMX7   PRELIMINARY;   PRT;   477 AA.
AC   Q6GMX7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073765; AAH73765.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Alignment Scores:
Pred. No.:   0.0971
Score: 81.30
Percent Similarity: 39.22%
Best Local Similarity: 33.33%
Query Match: 58.07%
DB:

Length: 477
Matches: 17
Conservative: 3
Mismatches: 4
Indels: 27
Gaps: 1

DELETED1 (1-81) x Q6GMX7 (1-477)

Qy   4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAGGAT 63
          ||||::||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   70 IleSerHisSerGlySerThrThrThrTyrAsnProSerLeuLysSerArgValThrLeuSer 89

Qy   64 ATT-- 66
          :::
Db   90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109

Qy   67 --AGCAGCTGG 75
                                                  |||||||||
Db   110 AlaValTyrTyrCysAlaHisGlySerSerTrp 120

RESULT 9
HV2I_HUMAN
ID   HV2I_HUMAN   STANDARD;   PRT;   146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; G1HUH2.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; signal.
FT   SIGNAL   1   19
FT   CHAIN   20   146   Ig heavy chain V-II region ARH-77.
FT   DOMAIN   20   117   V segment.
FT   DOMAIN   118   127   D segment.
FT   DOMAIN   128   146   J segment.
FT   DISULFID   42   115   By similarity.
FT   NON_TER   146   146
SQ   SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Alignment Scores:
Pred. No.:   0.207
Score: 78.40
Percent Similarity: 66.67%
Best Local Similarity: 62.96%
Query Match: 56.00%
DB:

Length: 146
Matches: 17
Conservative: 1
Mismatches: 3
Indels: 6
Gaps: 0

DELETED1 (1-81) x HV2I_HUMAN (1-146)

Qy   1 GAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   70 GluIleAsnHisSerGlySerThrAsnTyrLysThrSerLeuLysSerArgValThr--- 88

Qy   61 GATATTAGC 69
          |||||
Db   89 ---IleSer 90

RESULT 10
Q865X2

```
ID   Q86SX2        PRELIMINARY;      PRT;   139 AA.
AC   Q86SX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Full-length cDNA clone CS0DI004YM19 of B cells (Ramos cell line) of
DE   Homo sapiens (human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248300; CAD62627.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
SQ   SEQUENCE  139 AA;  15573 MW;  7D1E2302410E4F8C CRC64;

Alignment Scores:
Pred. No.:                        0.92
Score:                            73.70
Percent Similarity:               35.71%
Best Local Similarity:            30.36%
Query Match:                      52.64%
DB:                               2

DELETED1 (1-81) x Q86SX2 (1-139)

Qy    4 ATCAATCATAGTGGAAGCACCACCTACCAACCCGTCTCCTCAAGAGTCGGGCGAGT------  57
          ::|||||||| :::|||||||||||||||||||||||||||||||
Db   83 IleTyrTyrSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIleSer 102

Qy   57 ------------------------------------------------------------  57

Db  103 ValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThr 122

Qy   58 ---------------------------------CAGGATATTAGCAGC  72
                                          ||::|||||||
Db  123 AlaValTyrTyrCysAlaArgAspThrValArgGlyAspValSerSer 138
```

RESULT 11

```
ID   Q99M22        PRELIMINARY;      PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
```

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RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE  479 AA;  51992 MW;  768E39A138918892 CRC64;

Alignment Scores:
Pred. No.:                        1.55
Score:                            72.60
Percent Similarity:               33.93%
Best Local Similarity:            30.36%
Query Match:                      51.86%
DB:                               2

DELETED1 (1-81) x Q99M22 (1-479)

Qy    4 ATCAATCATAGTGGAAGCACCACCTACCAACCCGTCTCCTCAAGAGTCGGGCGAGTCA----  59
          |||||||| :::|| |||||||||||||||||||||||::::|||
Db   70 IleAsnTyrAspGlySerAsnAsnTyrAsnProSerLeuLysAsnArgIleSerIleThr  89

Qy   59 ------------------------------------------------------------  59

Db   90 ArgAspThrSerLysAsnGlnPhePheLeuLysLeuAsnSerValThrThrGluAspThr 109

Qy   60 --------------------------------GGATATTAGCAGCTGG  75
                                         |||||||    |||||
Db  110 AlaThrTyrTyrCysAlaSerArgArgGlyTyr----SerTrp 121
```

RESULT 12

```
ID   Q6GMX6        PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Alignment Scores:
Pred. No.: 1.87   Length: 465
Score: 72.00   Matches: 13
Percent Similarity: 80.00%   Conservative: 3
Best Local Similarity: 65.00%   Mismatches: 4
Query Match: 51.43%   Indels: 0
DB: 2   Gaps: 0

DELETED1 (1-81) x Q6GMX6 (1-465)

```
Qy  13 AGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGGAGTCAGGATATTAGCAGC 72
          |||||||||||||||||||||||||||||||||||||||||||  :::  :::
Db  73 SerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMetSerValAspThr 92
```

RESULT 13
Q96EY0
ID Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Alignment Scores:
Pred. No.: 1.95   Length: 620
Score: 72.00   Matches: 13
Percent Similarity: 80.00%   Conservative: 3
Best Local Similarity: 65.00%   Mismatches: 4
Query Match: 51.43%   Indels: 0
DB: 2   Gaps: 0

DELETED1 (1-81) x Q96EY0 (1-620)

```
Qy  13 AGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGGAGTCAGGATATTAGCAGC 72
          |||||||||||||||||||||||||||||||||||||||||||  :::  :::
Db  80 SerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMetSerValAspThr 99
```

RESULT 14
Q65ZI1
ID Q65ZI1 PRELIMINARY; PRT; 262 AA.
AC Q65ZI1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-HIV-1 reverse transcriptase single-chain variable.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hybridoma;
RX MEDLINE=96211469; PubMed=8648670;
RA Shaheen F., Duan Z., Zhu M., Bagasra O., Pomerantz R.J.;
RT "Targeting human immunodeficiency virus type 1 reverse transcriptase
RT by intracellular expression of single-chain variable fragments to
RT inhibit early stages of the viral life cycle.";
RL J. Virol. 70:3392-3400(1996).
DR EMBL; U48716; AAB64342.1; -.

DR   GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS0835; IG_LIKE; 2.
KW   RNA-directed DNA polymerase.
SQ   SEQUENCE 262 AA; 27842 MW; 7DF20138E53865E4 CRC64;

Alignment Scores:
Pred. No.:   2.7
Score: 70.60
Percent Similarity: 68.00%
Best Local Similarity: 64.00%
Query Match: 50.43%
DB: 2

Length: 262
Matches: 16
Conservative: 1
Mismatches: 4
Indels: 4
Gaps: 0

DELETED1 (1-81) x Q65ZI1 (1-262)

Qy   4 ATCAATCATAGTCGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAGGAT 63
          ||||||::||||||| || ||||||||||||||||||||||||||||| || ||
Db   198 IleAsnTyrSerGlyAspThrTyrTyrAsnProSerLeuLysSerArgIleSer----Il 216

Qy   64 ATTAGCA 70
          | |||
Db   216 eThrAla 218

RESULT 15
Q9UL73
ID   Q9UL73   PRELIMINARY;   PRT;   119 AA.
AC   Q9UL73;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035041; AAD56277.1; -.
DR   PIR; PH0876; PH0876.
DR   PIR; S12416; S12416.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS0835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   119   119
SQ   SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Alignment Scores:
Pred. No.:   3.66
Score: 69.30
Percent Similarity: 37.25%
Best Local Similarity: 29.41%
Query Match: 49.50%
DB: 2

Length: 119
Matches: 15
Conservative: 4
Mismatches: 5
Indels: 27
Gaps: 1

DELETED1 (1-81) x Q9UL73 (1-119)

Qy   4 ATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGGGCGAGTCAGGAT 63
          || :::|||||||||||||||||||||||||||||||||||| ::
Db   51 IleTyrTyrSerGlySerThrAsnTyrThrProSerLeuLysSerArgValThrIleSer 70

Qy   64 ATT-- 66
          :::
Db   71 ValAspArgSerLysAsnGlnPheSerLeuLysLeuThrSerLeuThrAlaAlaAspThr 90

Qy   67 -----------------------------------AGCAGCTGG 75
                                               |||::|||
Db   91 AlaValTyrPheCysAlaArgLeuSerAsnTrp 101

Search completed: August 4, 2005, 19:37:58
Job time : 113 secs

```
              GenCore version 5.1.6
     Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    August  4, 2005, 19:39:01 ; Search time 119 Seconds
                                       (without alignments)
                                       526.514 Million cell updates/sec

Title:            DELETED2
Perfect score:    140
Sequence:       1 CGGGCGAGTCAGGATATTAG.........ACAACCCGTCTCTCAAGAGT 81

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.1
                  Ygapop 10.0 , Ygapext  0.1
                  Fgapop  6.0 , Fgapext  0.1
                  Delop   6.0 , Delext   0.1

Searched:         2105692 seqs, 38676038l residues

Total number of hits satisfying chosen parameters:    4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=x1p
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3B/runat_04082005_120453_19604/app_query.fasta_1.263
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN 1 1 224 @runat_04082005_120453_19604 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :  A_Geneseq_16Dec04:*
        1:  geneseqp1980s:*
        2:  geneseqp1990s:*
        3:  geneseqp2000s:*
        4:  geneseqp2001s:*
        5:  geneseqp2002s:*
        6:  geneseqp2003as:*
        7:  geneseqp2003bs:*
        8:  geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100.1	71.5	253	5	ABP45322	Abp45322 Human BLy
2	100.1	71.5	253	7	ADG96149	Adg96149 Single ch
3	99.9	71.4	125	6	ADA89274	Ada89274 Human ant
4	98.2	70.1	80	2	AAW62794	Aaw62794 Amino aci
5	98.2	70.1	97	2	AAY05694	Aay05694 Multiple
6	98.2	70.1	97	5	ABG78212	Abg78212 Human Fv
7	98.2	70.1	97	6	ABG91903	Abg91903 Human ant
8	98.2	70.1	97	6	ABO27107	Abo27107 Human ger
9	98.2	70.1	97	7	ADB75646	Adb75646 Human pro
10	98.2	70.1	97	7	ADD28104	Add28104 Lymphoma
11	98.2	70.1	97	7	ADF10048	ADF10048 VEGF anti
12	98.2	70.1	97	7	ADF10150	ADF10150 Antibody
13	98.2	70.1	97	7	ADF09942	ADF09942 Antibody
14	98.2	70.1	97	7	ADJ80323	ADJ80323 VH gene 1
15	98.2	70.1	114	3	AAB01949	AAB01949 Anti-Id1
16	98.2	70.1	114	3	AAB01950	AAB01950 Anti-Id1
17	98.2	70.1	114	3	AAB01953	AAB01953 Anti-Id1
18	98.2	70.1	114	3	AAB01959	AAB01959 High affi
19	98.2	70.1	114	3	AAB01952	AAB01952 Anti-Id1
20	98.2	70.1	114	3	AAB01955	AAB01955 Strepativ
21	98.2	70.1	114	3	AAB01956	AAB01956 Strepativ
22	98.2	70.1	114	3	AAB01948	AAB01948 Wild-type
23	98.2	70.1	114	3	AAB01954	AAB01954 Anti-Id1
24	98.2	70.1	114	7	ADG70086	ADG70086 Diversifi
25	98.2	70.1	114	7	ADG70013	ADG70013 Diversifi
26	98.2	70.1	116	2	AAR66324	AAR66324 Human imm
27	98.2	70.1	117	4	AAM60904	AAM60904 Human bra
28	98.2	70.1	117	4	ABG55317	ABG55317 Human liv
29	98.2	70.1	117	5	ABG43454	ABG43454 Human pep
30	98.2	70.1	118	6	ADA89246	ADA89246 Human ant
31	98.2	70.1	122	7	ADK17418	ADK17418 Anti-huma
32	98.2	70.1	122	8	ADG42840	ADG42840 scFv Ab12
33	98.2	70.1	123	7	AAW03757	AAW03757 Anti-rhes
34	98.2	70.1	125	6	ADA89266	ADA89266 Human ant
35	98.2	70.1	139	3	AAY99556	AAY99556 Human LH1
36	98.2	70.1	139	6	ABR42859	ABR42859 Tumour-sp
37	98.2	70.1	139	6	ABW02445	ABW02445 Human mon
38	98.2	70.1	142	6	ABP96287	ABP96287 Anti-hTNF
39	98.2	70.1	154	6	ABP96293	ABP96293 Human ant
40	98.2	70.1	190	2	AAY34304	AAY34304 IgM antib
41	98.2	70.1	202	2	AAY34303	AAY34303 IgM antib
42	98.2	70.1	205	2	AAY34299	AAY34299 IgM antib
43	98.2	70.1	218	7	ADG70090	ADG70090 Diversifi
44	98.2	70.1	223	7	ADJ32112	ADJ32112 Human int
45	98.2	70.1	224	7	ADG70088	ADG70088 Diversifi

ALIGNMENTS

```
RESULT 1
ABP45322
ID   ABP45322 standard; protein; 253 AA.
XX
AC   ABP45322;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BlyS binding scFv SEQ ID 1333.
XX
KW   BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
```

PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1993-1994; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 253 AA;

Alignment Scores:
Pred. No.:   0.000258   Length: 253
Score: 100.10   Matches: 21
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.73%   Mismatches: 3
Query Match: 71.50%   Indels: 19
DB: 5   Gaps: 1

DELETED2 (1-81) x ABP45322 (1-253)

Qy   3 GGCGAGTCA--GGATAT 17
        |||||||| ||
Db 26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy 18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAA 77
        |||:::: ||||||||||||||||||||||||||||||||||||||||||||||||
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy 78 GAGT 81
        |||
Db 64 sSer 65

RESULT 2
ADG96149
ID   ADG96149 standard; protein; 253 AA.
XX
AC   ADG96149;
XX
DT   11-MAR-2004 (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 1333.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
OS   Unidentified.
XX
PN   WO2003055979-A2.
XX
PD   10-JUL-2003.
XX

PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLyS), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 1333; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 253 AA;

Alignment Scores:
Pred. No.:   0.000258   Length: 253
Score: 100.10   Matches: 21
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.73%   Mismatches: 3
Query Match: 71.50%   Indels: 19
DB: 7   Gaps: 1

DELETED2 (1-81) x ADG96149 (1-253)

Qy   3 GGCGAGTCA--GGATAT 17
        ||||||||| ||
Db 26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy 18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAA 77
        |||:::: ||||||||||||||||||||||||||||||||||||||||||||||||
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy 78 GAGT 81
        |||
Db 64 sSer 65

RESULT 3
ADA89274
ID   ADA89274 standard; protein; 125 AA.
XX
AC   ADA89274;
XX
DT   20-NOV-2003 (first entry)
XX
DE   Human antibody 3H2 heavy chain amino acid sequence SEQ ID NO:118.

```
Qy   25 ----------TGGTTAGCCGAAATCATCATAGTGGAAGCACCAACTACAACCCGTC 71
        ||||::    |||||||||||||||||||||||||||||||||||||||||||||
Db   44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64

Qy   72 TCTCAAGAGT 81
        ||||||||||
Db   64 rLeuLysSer 67

RESULT 4
AAW62794
ID   AAW62794 standard; peptide; 80 AA.
XX
AC   AAW62794;
XX
DT   23-SEP-1998  (first entry)
XX
DE   Amino acid sequence of a human antibody fragment.
XX
KW   Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW   inactivated endogenous Ig locus; B-cell development;
KW   human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW   kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW   production; antibody.
XX
OS   Homo sapiens.
XX
PN   WO9824893-A2.
XX
PD   11-JUN-1998.
XX
PF   03-DEC-1997;    97WO-US023091.
XX
PR   03-DEC-1996;    96US-00759620.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Jakobovits A,   Kucherlapati R,   Klapholz S,   Mendez M,   Green L;
XX
DR   WPI; 1998-333314/29.
XX
PT   New transgenic non-human mammals - having an inactivated immunoglobulin
PT   locus and a near complete human immunoglobulin locus, used for production
PT   of human antibodies.
XX
PS   Disclosure; Page 71; 128pp; English.
XX
CC   AAW62793-822 represent fragments of human antibodies produced by
CC   transgenic Xenomice, created using the method of the invention. The
CC   specification describes a transgenic non-human mammal which has genome
CC   modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC   locus, so that the mammal does not display normal B-cell development. The
CC   modified genome also has an inserted human heavy chain Ig locus in
CC   germline configuration, the human heavy chain Ig locus comprising a human
CC   micro constant region and regulatory and switch sequences, human J-H
CC   genes, human D-H genes, and human V-H genes and an inserted human kappa
CC   light chain Ig locus in germline configuration, the human kappa light
CC   chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC   and v-kappa genes, where the number of V-H and V-kappa genes inserted are
CC   selected to restore normal B-cell development in the mammal. The
CC   transgenic animals have a near complete human Ig locus, including both a
CC   human heavy chain locus and a human kappa light chain locus. They can be
CC   used for the production of human antibodies when exposed to particular
CC   antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC   will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
SQ   Sequence 80 AA;

Alignment Scores:
Pred. No.:                               Length:                   80
Score:                 0.000334          Matches:                  19
Percent Similarity:    98.20             Conservative:             2
Best Local Similarity: 65.62%            Mismatches:               3
                       59.38%
```

```
XX
KW   immunoglobulin; Ig; heavy chain variable domain;
KW   light chain variable domain; major histocompatibility complex; MHC;
KW   gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW   cancer.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200307O752-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003;   2003WO-US005128.
XX
PR   20-FEB-2002;   2002US-0358994P.
XX
PA   (DYAX-) DYAX CORP.
PA   (TECR ) TECHNION RES & DEV FOUND LTD.
XX
PI   Hoogenboom HRJM,  Reiter Y;
XX
DR   WPI; 2003-663847/62.
DR   N-PSDB; ADA89273.
XX
PT   New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT   and an immunoglobulin light chain variable (VL) domain, useful for
PT   preparing a composition for treating or preventing a cancerous disorder.
XX
PS   Disclosure; Fig 28B; 224pp; English.
XX
CC   The present invention describes a protein comprising an immunoglobulin
CC   (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC   domain. The protein binds a complex comprising a major histocompatibility
CC   complex (MHC) and a peptide, does not substantially bind the MHC in the
CC   absence of the bound peptide, and does not substantially bind the peptide
CC   in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC   MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC   comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC   comprising one or more nucleic acids for expressing the Ig that binds a
CC   complex having an MHC and a peptide, does not substantially bind the MHC
CC   in the absence of the bound peptide, and does not substantially bind the
CC   peptide in the absence of the MHC; (3) an isolated nucleic acid
CC   comprising a first segment that encodes the Ig variable domain; (4) a
CC   host cell comprising heterologous nucleic acid sequences that encodes the
CC   novel protein; (5) a transgenic animal whose genome includes heterologous
CC   nucleic acid sequences that encode the protein; (6) identifying the
CC   protein that specifically binds the MHC-peptide complex; (7) expressing
CC   an antigen-binding protein; (8) ablating or killing a target cell that
CC   displays a peptide on a surface MHC molecule; (9) treating or preventing
CC   a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC   complex in a sample. A protein of the invention has cytostatic activity,
CC   and can be used in gene therapy. The protein is useful for preparing a
CC   composition for treating or preventing a cancerous disorder. The present
CC   sequence represents the heavy chain of an antibody which binds to an MHC-
CC   peptide complex where the peptide component in as peptide fragment of
CC   hTERT.
XX
SQ   Sequence 125 AA;

Alignment Scores:
Pred. No.:                               Length:                   125
Score:                 0.000224          Matches:                  22
Percent Similarity:    99.90             Conservative:             1
Best Local Similarity: 50.00%            Mismatches:               2
Query Match:           47.83%            Indels:                   21
DB:                    71.36%            Gaps:                     1
                       6

DELETED2 (1-81) x ADA89274 (1-125)

Qy    3 GGCGAGTCAGGATATTAGCAGC---------------------------------- 24
        |||   ||| ||||||||||||||
Db   26 GlyGlySer----IleSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44
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Query Match: 70.14%   Indels: 8
DB: 2   Gaps: 0

DELETED2 (1-81) x AAW62794 (1-80)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
        ||::: ||| |||||||||||||||||||||||||||||
Db   25 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 42

Qy   62 ACAACCCGTCTCTCAAGAGT 81
        ||||||||||||||||||||
Db   42 yrAsnProSerLeuLysSer 48

RESULT 5
AAY05694
ID   AAY05694 standard; protein; 97 AA.
XX
AC   AAY05694;
XX
DT   19-JUL-1999 (first entry)
XX
DE   Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
XX
KW   Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
KW   heavy chain variable region; VH gene; somatic hypermutation;
KW   B-cell clonality; RA gene; diagnosis; human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   1..30
FT   /label= FR1
FT   Misc-difference 8
FT   /note= "encoded by GGC"
FT   Misc-difference 13
FT   /note= "replaces Glu of RA"
FT   Misc-difference 14
FT   /note= "encoded by CCT"
FT   Misc-difference 23
FT   /note= "replaces Gly of RA"
FT   Misc-difference 25
FT   /note= "replaces Phe of RA"
FT   Misc-difference 30
FT   /note= "replaces Gly of RA"
FT   Region   31..36
FT   /label= CDR1
FT   Misc-difference 31
FT   /note= "replaces Gly of RA"
FT   Misc-difference 32
FT   /note= "replaces Phe of RA"
FT   Region   37..50
FT   /label= FR2
FT   Region   51..66
FT   /label= CDR2
FT   Misc-difference 56
FT   /note= "replaces Asn of RA"
FT   Misc-difference 57
FT   /note= "replaces Ser of RA"
FT   Misc-difference 58
FT   /note= "replaces Lys of RA"
FT   Region   67..97
FT   /label= FR3
FT   Misc-difference 71
FT   /note= "replaces Leu of RA"
FT   Misc-difference 81
FT   /note= "replaces Arg of RA"
XX
PN   WO9915696-A1.
XX
PD   01-APR-1999.
XX
PF   17-SEP-1998; 98WO-CA000873.
XX

PR   19-SEP-1997; 97CA-02216595.
PR   04-NOV-1997; 97CA-0220245.
XX
PA   (QINY/) QIN Y.
PI   Qin Y;
XX
DR   WPI; 1999-276985/23.
DR   N-PSDB; AAX25318.
XX
PT   Determination of B-cell clonality by amplification or enzymatic
PT   digestion.
XX
PS   Disclosure; Fig 9D; 67pp; English.
XX
CC   This sequence represents a heavy chain variable region (VH) as predicted
CC   from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
CC   fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
CC   B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
CC   in nucleotide and predicted amino acid (see AAY05691-94) sequences were
CC   compared with the closest known germline VH genes; for 4d76, this was RA.
CC   The results provided direct evidence that intrathecal clonally expanded B
CC   -cells from the CSF of MS patients are hypermutated postgerminal centre
CC   antibody-forming or memory lymphocytes that havd undergone antigen
CC   selection. This finding implicates an important pathogenic pathway for
CC   the development of demyelination in CNS of MS. The invention provides
CC   assay kits for determining B-cell or T-cell clonality. This technology
CC   allows the establishment of clonal specific RNA library from pathogenic
CC   cells in the CNS of patients, which is important for further
CC   understanding of the role of antigen(s) in the cause of B-cell clonal
CC   expansion, and towards developing antigen specific therapeutic strategy
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.000353   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 2   Gaps: 0

DELETED2 (1-81) x AAY05694 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
        ||::: ||| ::: |||||||||||||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
        ||||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 6
ABG78212
ID   ABG78212 standard; protein; 97 AA.
XX
AC   ABG78212;
XX
DT   15-NOV-2002 (first entry)
XX
DE   Human Fv molecule hypervariable region related peptide #87.
XX
KW   Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW   disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW   lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200259264-A2.
XX
PD   01-AUG-2002.
XX
PF   31-DEC-2001; 2001WO-US049440.
XX

```
XX
PR   29-DEC-2000; 2000US-0075181.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI   Plaksin D, Peretz T;
XX
DR   WPI; 2002-619166/66.
XX
PT   Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT   or fragment, or construct of fragment with enhanced binding
PT   characteristics so as to selectively bind target cell in favor of other
PT   cells.
XX
PS   Claim 13; Page 193; 232pp; English.
XX
CC   The invention relates to a peptide or polypeptide comprising an Fv
CC   molecule, a construct or fragments or a construct of a fragment with
CC   enhanced binding characteristics which selectively and/or specifically
CC   binds to a target cell in favour of other cells, where binding is
CC   primarily determined by a first hypervariable region and Fv is a single
CC   chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC   association with or attached, coupled, combined, linked to or fused to a
CC   pharmaceutical agent, is useful in the manufacture of a medicament, where
CC   the medicament has activity against a diseased cell, preferably a cancer
CC   cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC   myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC   acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC   composition for use in inhibiting the growth of a diseased or cancer
CC   cell. This sequence represents a human Fv molecule hypervariable region
CC   related peptide of the invention
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:                0.000353        Length:         97
Score:                    98.20           Matches:        19
Percent Similarity:       65.62%          Conservative:   2
Best Local Similarity:    59.38%          Mismatches:     3
Query Match:              70.14%          Indels:         8
DB:                       5               Gaps:           0

DELETED2 (1-81) x ABG78212 (1-97)

Qy    2 GGGCGAGTCAGGATATTATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
           ||| |||::   ||         |||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCCAAGAGT 81
          ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 7
ABG91903
ID   ABG91903 standard; protein; 97 AA.
XX
AC   ABG91903;
XX
DT   04-DEC-2002 (first entry)
XX
DE   Human antibody fragment #87.
XX
KW   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW   metastasis; hypervariable region; autoimmune disease; thrombosis;
KW   restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW   myocardial infarction; retinopathic disease; abnormal platelet function;
KW   sulphated tyrosine-dependent protein-protein interaction.
XX
OS   Homo sapiens.
XX
PN   WO200253700-A2.
XX
```

```
PD   11-JUL-2002.
XX
PF   31-DEC-2001; 2001WO-US049442.
XX
PR   29-DEC-2000; 2000US-0075181.
PR   29-DEC-2000; 2000US-0258948P.
XX
PA   (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI   Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI   Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR   WPI; 2002-674776/72.
XX
PT   Novel isolated epitope present on cancer cells and important in
PT   physiological phenomena such as cell rolling, metastasis and
PT   inflammation, for treating autoimmune, inflammatory or cardiovascular
PT   diseases, and cancer.
XX
PS   Disclosure; Page 269; 0pp; English.
XX
CC   The invention relates to an isolated epitope present on cancer cells and
CC   important in physiological phenomena such as cell rolling, metastasis and
CC   inflammation, where the epitope is capable of being bound by an antibody,
CC   its antigen-binding fragment or its complex comprising at least one
CC   antibody or its binding fragment having a first hypervariable region. The
CC   epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC   disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC   tumour or leukaemia cells, increase in number of tumour or leukaemia
CC   cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC   platelet and/or cell-platelet adhesion or aggregation, for increasing
CC   mortality of tumour or leukaemia cells, for increasing the susceptibility
CC   of diseased cells to damage by anti-disease, anti-cancer or anti-
CC   leukaemia agents, or for decreasing the number of tumour or leukaemia
CC   cells in a patient, or in the manufacture of a medicament for the above
CC   mentioned purposes. The epitopes are useful for diagnosing and treating
CC   diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC   diseases, cardiovascular diseases such as myocardial infarction,
CC   retinopathic diseases and other diseases mediated by abnormal platelet
CC   function and diseases caused by sulphated tyrosine-dependent protein-
CC   protein interactions. This sequence represents a human antibody fragment
CC   of the invention
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:                0.000353        Length:         97
Score:                    98.20           Matches:        19
Percent Similarity:       65.62%          Conservative:   2
Best Local Similarity:    59.38%          Mismatches:     3
Query Match:              70.14%          Indels:         8
DB:                       5               Gaps:           0

DELETED2 (1-81) x ABG91903 (1-97)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
           ||| ::   ||        |||:::     ||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCCAAGAGT 81
          |||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 8
ABG27107
ID   ABG27107 standard; protein; 97 AA.
XX
AC   ABG27107;
XX
DT   10-SEP-2003 (first entry)
XX
DE   Human germline heavy chain variable region gene segment #40.
XX
```

```
KW   Human; heavy chain variable region; VH; humanised antibody;
KW   chimeric antibody; complementarity determining region; CDR;
KW   canonical CDR structure type.
XX
OS   Homo sapiens.
XX
PN   US2003039649-A1.
XX
PD   27-FEB-2003.
XX
PF   12-JUL-2002; 2002US-00194975.
XX
PR   12-JUL-2001; 2001US-0305111P.
XX
PA   (FOOT/) FOOTE J.
XX
PI   Foote J;
XX
DR   WPI; 2003-492151/46.
XX
PT   Making humanised antibody for converting antibody, by making chimeric
PT   antibodies containing complementarity determining region from non-human
PT   antibody and appropriate framework sequences of human antibodies.
XX
PS   Example 1; Fig 1; 31pp; English.
XX
CC   The invention describes a method of making a humanised antibody,
CC   comprising making chimeric antibodies containing a complementarity
CC   determining region (CDR) from a non-human antibody and appropriate
CC   framework sequences (I) of human antibodies. (I) is selected by using
CC   canonical CDR structure types of human antibodies in comparison to
CC   germline canonical CDR structure types of non-human antibodies as the basis
CC   for selection, for humanisation. The method is useful for making a
CC   humanised antibody or a converted antibody. The method is applicable for
CC   converting a subject antibody sequence of any subject species to a less
CC   immunogenic form suitable for use in an object species. The method is
CC   reliable for identifying suitable human framework sequences to support
CC   non-human CDR regions and to provide humanised antibodies that retain
CC   high antigen binding with low immunogenicity in humans, without the need
CC   for direct comparison of framework sequences, without the need for
CC   determining critically important amino acid residues in the framework,
CC   and without the need for multiple iteration and construction to obtain
CC   humanised antibodies with suitable therapeutic properties. The antibody
CC   has high affinity and low immunogenicity without need for comparing
CC   framework sequences between non-human and human antibodies. This sequence
CC   represents a human heavy chain variable region gene segment used in the
CC   creation of humanised antibodies
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.000353        Length:          97
Score:                 98.20           Matches:         19
Percent Similarity:    65.62%          Conservative:     2
Best Local Similarity: 59.38%          Mismatches:       3
Query Match:           70.14%          Indels:           8
DB:                     6              Gaps:             0

DELETED2 (1-81) x ABO27107 (1-97)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCCAAATCAATCATAGTGGAAGCACCAACT 61
          ||:::   |||   ||||||||||||||||||||||||
Db   42 GlyLeu---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCCAAGAGT 81
          ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 9
ADB75646
ID   ADB75646 standard; protein; 97 AA.
XX
AC   ADB75646;
```

```
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human protein relating to the invention SEQ ID NO:55.
XX
KW   antibody library; CD1 region; CD2 region; VH region; VL region;
KW   immunoglobulin; CD3 region; TM1 scFv; human.
XX
OS   Homo sapiens.
XX
PN   WO200304198-A1.
XX
PD   30-MAY-2003.
XX
PF   22-NOV-2002; 2002WO-JP012236.
XX
PR   22-NOV-2001; 2001JP-00358602.
XX
PA   (UYKE-) UNIV KEIO.
XX
PI   Shimizu N, Takayanagi A, Okui M;
XX
DR   WPI; 2003-449818/42.
XX
PT   Highly stable artificial antibody libraries with super-repertory and
PT   little contamination from unexpressible ones, useful as tool in
PT   proteomics and e.g. for diagnosis and treating various diseases.
XX
PS   Disclosure; Page 101; 108pp; Japanese.
XX
CC   The invention relates to a novel artificial single-stranded antibody
CC   library with superior-repertory. The library is created by using a cDNA
CC   library as template for amplifying a fragment containing the CD1 and CD2
CC   regions of the VH or VL region of immunoglobulin gene and a fragment
CC   containing the CD3 region by PCR, respectively, producing VH and VL
CC   libraries, transferring into a host, and displaying the single-stranded
CC   antibody on a phage surface. An antibody library of the invention is
CC   useful as a tool in proteomics and antibody chips and filters, for
CC   screening ligands for antigens, and for studying protein-DNA interaction,
CC   diagnosis and treating various diseases. The present sequence represents
CC   a protein of the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. NO.:              0.000353        Length:          97
Score:                 98.20           Matches:         19
Percent Similarity:    65.62%          Conservative:     2
Best Local Similarity: 59.38%          Mismatches:       3
Query Match:           70.14%          Indels:           8
DB:                     7              Gaps:             0

DELETED2 (1-81) x ADB75646 (1-97)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||:::   |||   ||||||||||||||||||||||||
Db   42 GlyLeu---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCCAAGAGT 81
          ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 10
ADD28104
ID   ADD28104 standard; protein; 97 AA.
XX
AC   ADD28104;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Lymphoma related immunoglobulin variable region F5.
XX
KW   B-cell; malignant; immunoglobulin; immunoglobulin variable region;
```

KW   Ig variable region; glycosylation site; lymphoma; B cell receptor;
KW   cytostatic; gene therapy; glycosylation inhibitor;
KW   non-Hodgkin's lymphoma.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003074059-A2.
XX
PD   12-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-GB000783.
XX
PR   07-MAR-2002; 2002GB-00005395.
XX
PA   (CANC-) CANCER RES TECHNOLOGY LTD.
XX
PI   Zhu D, Stevenson F;
XX
DR , WPI; 2003-902720/82.
XX
PT   Classifying a B-cell as malignant or normal by isolating a sequence
PT   representing an Ig variable region from the B cell, detecting the
PT   presence of a glycosylation site and classifying the cell as malignant or
PT   normal.
XX
PS   Disclosure; Fig 4; 61pp; English.
XX
CC   The present invention describes a method for classifying a B-cell as
CC   malignant or normal comprising: (a) isolating a sequence representing an
CC   immunoglobulin (Ig) variable region from the B cell; (b) detecting the
CC   presence of a glycosylation site; and (c) classifying the cell as
CC   malignant or normal on the basis of the presence or absence of a
CC   glycosylation site. Also described: (1) treating a patient suffering from
CC   or at risk of having lymphoma; (2) screening for substances capable of
CC   inhibiting glycosylation of the Ig variable region of the B cell receptor
CC   ; and (3) screening for substances (S) capable of inhibiting the
CC   interaction between lectins of the type found in the germinal centre and
CC   N-glycans found on the surface of Ig of lymphoma cells. (S) has
CC   cytostatic activity, and can be used in gene therapy, and as a
CC   glycosylation inhibitor. The method is useful in classifying a B-cell as
CC   malignant or normal. The glycosylation inhibitor is useful in preparing a
CC   medicament for treating non-Hodgkin's lymphoma. The present sequence
CC   represents an Ig variable region sequence which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 97 AAs;

Alignment Scores:
Pred. No.:   0.000353   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 7   Gaps: 0

DELETED2 (1-81) x ADD28104 (1-97)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
       ||::: || |||||||||||||||||||||||||||
Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy 62 ACAACCCGTCTCTCCAAGAGT 81
       |||||||||||||||||
Db 59 yrAsnProSerLeuLysSer 65

RESULT 11
ADF10048
ID   ADF10048 standard; protein; 97 AA.
XX
AC   ADF10048;
XX
DT   12-FEB-2004 (first entry)

XX
DE   VEGF antibody heavy chain variable region VH_4-34.
XX
KW   Antibody; stability; solubility; antigen binding affinity;
KW   variable region; human; VEGF.
XX
OS   Homo sapiens.
XX
PN   WO2003074679-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
PS   Example 6; Fig 16a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:   0.000353   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 7   Gaps: 0

DELETED2 (1-81) x ADF10048 (1-97)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
       ||::: || |||||||||||||||||||||||||||
Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy 62 ACAACCCGTCTCTCCAAGAGT 81
       |||||||||||||||||
Db 59 yrAsnProSerLeuLysSer 65

RESULT 12
ADF10150
ID   ADF10150 standard; protein; 97 AA.
XX
AC   ADF10150;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Antibody heavy chain variable region VH_4-34.

Column 1 (RESULT 13)

```
XX
KW   Antibody; stability; solubility; antigen binding affinity;
KW   variable region; human.
XX
OS   Homo sapiens.
XX
PN   WO2003074679-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
PS   Example 16; Fig 40a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position(s); analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;
XX

Alignment Scores:
Pred. No.:              97           Length:          97
Score:                  98.20        Matches:         19
Percent Similarity:     65.62%       Conservative:    2
Best Local Similarity:  59.38%       Mismatches:      3
Query Match:            70.14%       Indels:          8
DB:                                  Gaps:            0

DELETED2 (1-81) x ADF10150 (1-97)

Qy     2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCCAAATCAATCATAGTGGAAGCACCAACT  61
             |||:::   ||   |||:::|||||||||||||||||
Db    42  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  59

Qy    62  ACAACCCGTCTCTCAAGAGT  81
             ||||||||||||||
Db    59  yrAsnProSerLeuLysSer  65

RESULT 13
ADF09942
ID   ADF09942 standard; protein; 97 AA.
XX
AC   ADF09942;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Antibody heavy chain variable region VH_4-34.
XX
KW   Antibody; stability; solubility; antigen binding affinity;
```

Column 2 (RESULT 14)

```
KW   Antibody; stability; solubility; antigen binding affinity;
KW   variable region; human.
XX
OS   Homo sapiens.
XX
PN   WO2003074679-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-US006598.
XX
PR   01-MAR-2002; 2002US-0360843P.
PR   29-MAY-2002; 2002US-0384197P.
XX
PA   (XENC-) XENCOR.
XX
PI   Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR   WPI; 2003-722066/68.
XX
PT   Computer optimization of physicochemical properties of antibodies
PT   comprises analyzing the interactions of amino acids at variable
PT   positions.
XX
PS   Disclosure; Fig 2a; 135pp; English.
XX
CC   The present invention relates to a method for optimizing at least one
CC   physico-chemical property of an antibody by a computational screening
CC   method. The method comprises: receiving a template antibody structure;
CC   selecting at least one variable position belonging to the antibody
CC   structure; selecting at least one amino acid to be considered at the
CC   variable position; analyzing the interaction of each selected amino
CC   acid at each variable position with at least part of the remainder of the
CC   antibody, including the selected amino acids at other variable positions;
CC   and identifying a set of at least one antibody sequence with at least one
CC   optimized physico-chemical property. The method is useful for optimizing
CC   the physico-chemical properties of an antibody, especially the stability,
CC   solubility, or antigen binding affinity. The optimized antibody may be
CC   useful for treating a patient. The present sequence is an antibody
CC   variable region sequence used to illustrate the invention.
XX
SQ   Sequence 97 AA;
XX

Alignment Scores:
Pred. No.:              97           Length:          97
Score:                  98.20        Matches:         19
Percent Similarity:     65.62%       Conservative:    2
Best Local Similarity:  59.38%       Mismatches:      3
Query Match:            70.14%       Indels:          8
DB:                                  Gaps:            0

DELETED2 (1-81) x ADF09942 (1-97)

Qy     2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCCAAATCAATCATAGTGGAAGCACCAACT  61
             |||:::   ||   |||:::|||||||||||||||||
Db    42  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  59

Qy    62  ACAACCCGTCTCTCAAGAGT  81
             ||||||||||||||
Db    59  yrAsnProSerLeuLysSer  65

RESULT 14
ADJ80323
ID   ADJ80323 standard; protein; 97 AA.
XX
AC   ADJ80323;
XX
DT   06-MAY-2004 (first entry)
XX
DE   VH gene locus antibody amino acid sequence #43.
XX
KW   hybrid antibody; antibody; framework region; homology; immunogenicity.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200304B321-A2.
XX
PD   12-JUN-2003.
XX
PF   03-DEC-2002; 2002WO-US038450.
XX
PR   03-DEC-2001; 2001US-0336591P.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Rother R, Wu D;
XX
DR   WPI; 2003-513753/48.
XX
PT   Producing a hybrid antibody or hybrid antibody fragment by operatively
PT   linking the selected framework sequences to one or more complementarity
PT   determining regions of the initial antibody.
XX
PS   Disclosure; SEQ ID NO 83; 77pp; English.
XX
CC   The invention relates to a method of producing a hybrid antibody or
CC   hybrid antibody fragment by: (i) providing an initial antibody having
CC   specificity for a target; (ii) determining the sequence of a variable
CC   region of the initial antibody; (iii) selecting a first component of the
CC   variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
CC   sequence of the first component to sequencers contained in a reference
CC   database of antibody sequences or antibody fragment sequences from a
CC   target species; (v) selecting a sequence from an antibody in the database
CC   which demonstrates a high degree of homology to the first component; (vi)
CC   selecting a second component of the variable region which is different
CC   than the first component, the second component selected from the group
CC   consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
CC   second component to sequences contained in a reference database of
CC   antibody sequences or antibody fragment sequences from the target species
CC   ; (viii) selecting a sequence from the database which demonstrates a high
CC   degree of homology to the second component and which is from a different
CC   antibody than the selected antibody; and (ix) operatively linking the
CC   selected framework sequences to one or more complementarity determining
CC   regions (CDRs) of the initial antibody to produce a hybrid antibody or
CC   hybrid antibody fragment. The method is useful for producing a hybrid
CC   antibody or hybrid antibody fragment (claimed). The antibody and
CC   fragments are useful for therapeutic and diagnostic purposes. The method
CC   uses entire framework regions from a single antibody variable heavy or
CC   variable light chain to receive the CDRs. This produces antibodies that
CC   are highly homologous and exhibit reduced immunogenicity while
CC   maintaining an optimum binding profile. This sequence represents the
CC   amino acid sequence of an antibody from the VH gene locus.
XX
SQ   Sequence 97 AA;

Alignment Scores:
Pred. No.:              0.000353      Length:          97
Score:                  98.20         Matches:         19
Percent Similarity:     65.62%        Conservative:    2
Best Local Similarity:  59.38%        Mismatches:      3
Query Match:            70.14%        Indels:          8
DB:                     7             Gaps:            0

DELETED2 (1-81) x ADJ80323 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCCAGCTGGTTAGCCGGAAATCAATCATCAGTCGGAAGCACCAACT 61
         ||:|::    ||       ||||:|| |||||||||||||||||||||||||
Db  42 GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy  62 ACAACCGTCCTCTCAAGAGT 81
         ||||||||||||||||||
Db  59 yrAsnProSerLeuLysSer 65
```

```
AC   AAB01949;
XX
DT   18-SEP-2000 (first entry)
XX
DE   Anti-Id1 Ab binding-defective mutant Ramos cell VH K70N/S77N.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; heavy chain variable region; VH;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key          Location/Qualifiers
FT   Misc-difference 71
FT                /note= "Encoded by CAG"
XX
PN   WO200022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;  99WO-GB003358.
XX
PR   09-OCT-1998;  98GB-00022104.
PR   19-JAN-1999;  99GB-00001141.
PR   09-JUN-1999;  99GB-00013435.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Sale JE, Neuberger MS, Cumbers SJ;
XX
DR   WPI; 2000-317971/27.
DR   N-PSDB; AAA52435.
XX
PT   Lymphoid cell line preparation useful for producing gene products having
PT   desired activity, involves screening and selecting cells having ongoing
PT   target sequence diversification and higher mutation rates.
XX
PS   Example 5; Page; 69pp; English.
XX
CC   The invention relates to a method of preparing a lymphoid cell line
CC   capable of capable of directed constitutive hypermutation of a target
CC   nucleic acid region. The method comprises screening a cell population for
CC   ongoing target sequence diversification and selecting a cell in which the
CC   rate of target nucleic acid mutation exceeds that of other nucleic acid
CC   mutation by a factor of 100 or more. The invention also relates to a
CC   method for preparing a gene product with a desired activity, comprising
CC   expressing a nucleic acid encoding the target gene operably linked to a
CC   sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC   transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC   cells which express a mutated gene product with the desired activity. One
CC   or more clonal populations of the identified cells is established, and
CC   cells with an improved activity of interest are selected. These steps may
CC   be iteratively repeated until a gene product with a desired of activity
CC   is obtained. The cell lines prepared according to the method of the
CC   invention are used for directed constitutive hypermutation of a nucleic
CC   acid region in the preparation of a gene product, preferably an enzyme or
CC   an immunoglobulin (Ig) with a desired activity. In the exemplifications
CC   of the invention, IgM-secreting Ramos cells were selected for use as they
CC   undergo hypermutation during clonal expansion. This was determined on the
CC   basis of the amount of diversity in the heavy chain variable region (VH).
CC   Sequences AAB01949-B01954 represent various mutant Ramos cell IgM VHs
CC   (AAB01949-B01954) which have lost the ability to bind anti-idiotype
CC   antibodies (anti-Id1 Ab) relative to the wild-type VH (AAB01948). Note:
CC   The present sequence is not shown in the specification, but is derived
CC   from the wild-type Ramos cell VH shown in figure 7
XX
SQ   Sequence 114 AA;

Alignment Scores:
Pred. No.:       0.00037        Length:          114

RESULT 15
AAB01949
ID   AAB01949 standard; protein; 114 AA.
XX
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Score:                  98.20          Matches:       19
Percent Similarity:     65.62%         Conservative:   2
Best Local Similarity:  59.38%         Mismatches:     3
Query Match:            70.14%         Indels:         8
DB:                     3              Gaps:           0

DELETED2 (1-81) x AAB01949 (1-114)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          |||::::    |||       |||:::    ||||||||||||||||||||||||||||
Db   36 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 53

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||||||||||
Db   53 yrAsnProSerLeuLysSer 59


Search completed: August  4, 2005, 20:00:48
Job time : 123 secs
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     August  4, 2005, 19:53:13 ; Search time 29.5 Seconds
                                        (without alignments)
                                        409.937 Million cell updates/sec

Title:      DELETED2
Perfect score: 140
Sequence:   1 CGGGCGAGTCAGGATATTAG........ACAACCGTCTCTCAAGAGT 81

Scoring table: BLOSUM62
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            Ygapop 10.0 , Ygapext  0.1
            Fgapop  6.0 , Fgapext  0.1
            Delop   6.0 , Delext   0.1

Searched:   513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters:    1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN_1_1_46 @runat_04082005_120454_19634_19634 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :  Issued_Patents_AA:*
1:  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2:  /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3:  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4:  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	98.2	70.1	116	3	US-08-545-809A-118	Sequence 118, App
2	98.2	70.1	123	4	US-08-793-450-4	Sequence 4, Appli
3	98.2	70.1	139	4	US-09-203-768A-2	Sequence 2, Appli
4	98.2	70.1	472	3	US-08-793-450-8	Sequence 8, Appli
5	93.2	66.6	429	4	US-09-372-425A-6	Sequence 6, Appl
6	92.1	65.8	118	3	US-09-025-769B-25	Sequence 25, Appl
7	92.1	65.8	118	4	US-09-490-070A-25	Sequence 25, Appl
8	92.1	65.8	118	4	US-09-490-153-25	Sequence 25, Appl
9	92.1	65.8	118	4	US-09-490-324-25	Sequence 25, Appl
10	91.1	65.1	120	3	US-08-545-809A-137	Sequence 137, App
11	87.2	62.3	147	4	US-09-471-276-835	Sequence 835, App
12	86.3	61.6	130	3	US-08-466-151-5	Sequence 5, Appli
13	86.3	61.6	130	3	US-08-466-163B-5	Sequence 5, Appli
14	86.3	61.6	130	4	US-09-802-096-5	Sequence 5, Appli
15	86.3	61.6	130	4	US-09-802-077-5	Sequence 5, Appli
16	85.2	60.9	447	2	US-09-372-425A-2	Sequence 2, Appli
17	83.1	59.4	118	2	US-08-652-816A-13	Sequence 13, Appl
18	83.1	59.4	139	4	US-09-471-276-837	Sequence 837, App
19	83.1	59.4	244	3	US-08-918-148-79	Sequence 79, Appl
20	83.1	59.4	244	4	US-09-138-091A-77	Sequence 77, Appl
21	81.2	58.0	119	2	US-08-428-197-16	Sequence 16, Appl
22	81.2	58.0	119	5	PCT-US93-10555-16	Sequence 16, Appl
23	80.1	57.2	100	4	US-09-726-219A-169	Sequence 169, App
24	80.1	57.2	117	3	US-09-720-493-2	Sequence 2, Appli
25	79.3	56.6	100	2	US-08-273-146-69	Sequence 69, Appl
26	79.3	56.6	137	3	US-08-466-151-7	Sequence 7, Appli
27	79.3	56.6	137	4	US-08-466-163B-7	Sequence 7, Appli
28	79.3	56.6	137	4	US-09-802-096-7	Sequence 7, Appli
29	79.3	56.6	137	4	US-09-802-077-7	Sequence 7, Appli
30	79.1	56.5	119	3	US-09-025-769B-39	Sequence 39, Appl
31	79.1	56.5	119	3	US-09-025-769B-65	Sequence 65, Appl
32	79.1	56.5	119	4	US-09-490-070A-39	Sequence 39, Appl
33	79.1	56.5	119	4	US-09-490-070A-65	Sequence 65, Appl
34	79.1	56.5	119	4	US-09-490-153-39	Sequence 39, Appl
35	79.1	56.5	119	4	US-09-490-153-65	Sequence 65, Appl
36	79.1	56.5	119	4	US-09-490-324-39	Sequence 39, Appl
37	79.1	56.5	119	4	US-09-490-324-65	Sequence 65, Appl
38	78.3	55.9	118	4	US-09-343-698-6	Sequence 6, Appli
39	78.3	55.9	118	4	US-08-325-955-6	Sequence 6, Appli
40	78.3	55.9	119	3	US-08-767-128-18	Sequence 18, Appl
41	78.3	55.9	213	4	US-09-170-769A-2	Sequence 2, Appli
42	78.3	55.9	832	3	US-08-630-820-7	Sequence 7, Appli
43	78.3	55.9	832	4	US-09-277-453-7	Sequence 7, Appli
44	78.1	55.8	116	3	US-08-545-809A-140	Sequence 140, App
45	77.9	55.6	76	3	US-08-851-362D-22	Sequence 22, Appl

ALIGNMENTS

```
RESULT 1
US-08-545-809A-118
; Sequence 118, Application US/0854580 9A
; Patent No. 6096878
GENERAL INFORMATION:
   APPLICANT: Honjo, Tasuku
   APPLICANT: Matsuda, Fumihiko
   TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
   TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
   NUMBER OF SEQUENCES: 145
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: Fish & Richardson, P.C.
     STREET: 225 Franklin Street
     CITY: Boston
     STATE: MA
     COUNTRY: US
     ZIP: 02110-2804
   COMPUTER READABLE FORM:
     MEDIUM TYPE: Diskette
     COMPUTER: IBM Compatible
     OPERATING SYSTEM: Windows95
     SOFTWARE: FastSBQ for Windows Version 2.0
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/545,809A
     FILING DATE: 27-MAR-1996
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER: PCT/JP93/00603
     FILING DATE: 10-MAY-1993
   ATTORNEY/AGENT INFORMATION:
     NAME: Freeman, John W.
     REGISTRATION NUMBER: 29,066
     REFERRNCE/DOCKET NUMBER: 06501/004001
   TELECOMMUNICATION INFORMATION:
     TELEPHONE: 617-542-5070
     TELEFAX: 617-542-8906
     TELEX: 200154
```

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;   INFORMATION FOR SEQ ID NO: 118:
;      SEQUENCE CHARACTERISTICS:
;         LENGTH: 116 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-545-809A-118

Alignment Scores:
Pred. No.:                4.16e-05          Length:              116
Score:                    98.20             Matches:             19
Percent Similarity:       65.62%            Conservative:        2
Best Local Similarity:    59.38%            Mismatches:          3
Query Match:              70.14%            Indels:              8
DB:                       3                 Gaps:                0

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Qy      2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT  61
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Db     61  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  78

Qy     62  ACAACCCGTCTCTCAAGAGT  81
           ||||||||||||||||||
Db     78  yrAsnProSerLeuLysSer  84

RESULT 2
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
;    APPLICANT: EDELMAN, LENA
;    APPLICANT: MARGARITTE, CHRISTEL
;    APPLICANT: KACZOREK, MICHEL
;    APPLICANT: CHAABIHI, HASSAN
;    TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES: 25
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;       ADDRESSEE: P.C.
;       STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;       CITY: ARLINGTON
;       STATE: VA
;       COUNTRY: USA
;       ZIP: 22202
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/793,450
;       FILING DATE: 03-MAR-1997
;       CLASSIFICATION: 536
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: FR 94/10566
;       FILING DATE: 02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;       NAME: OBLON, NORMAN F.
;       REGISTRATION NUMBER: 24,618
;       REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 703-413-3000
;       TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 4:
;      SEQUENCE CHARACTERISTICS:
;         LENGTH: 123 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-793-450-4

Alignment Scores:
Pred. No.:                4.25e-05          Length:              123
Score:                    98.20             Matches:             19
Percent Similarity:       65.62%            Conservative:        2
Best Local Similarity:    59.38%            Mismatches:          3
Query Match:              70.14%            Indels:              8
DB:                       3                 Gaps:                0

DELETED2 (1-81) x US-08-793-450-4 (1-123)

Qy      2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT  61
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Db     42  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  65

Qy     62  ACAACCCGTCTCTCAAGAGT  81
           ||||||||||||||||||
Db     59  yrAsnProSerLeuLysSer  65

RESULT 3
US-09-203-768A-2
; Sequence 2, Application US/0920376 8A
; Patent No. 6787638
; GENERAL INFORMATION:
;    APPLICANT: Huse, William D.
;    APPLICANT: Watkins, Jeffry D.
;    TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
;    TITLE OF INVENTION: of Use
;    FILE REFERENCE: P-IX 2947
;    CURRENT APPLICATION NUMBER: US/09/203,768A
;    CURRENT FILING DATE: 1998-12-02
;    NUMBER OF SEQ ID NOS: 8
;    SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 2
;      LENGTH: 139
;      TYPE: PRT
;      ORGANISM: Homo sapiens
US-09-203-768A-2

Alignment Scores:
Pred. No.:                4.45e-05          Length:              139
Score:                    98.20             Matches:             19
Percent Similarity:       65.62%            Conservative:        2
Best Local Similarity:    59.38%            Mismatches:          3
Query Match:              70.14%            Indels:              8
DB:                       4                 Gaps:                0

DELETED2 (1-81) x US-09-203-768A-2 (1-139)

Qy      2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT  61
              |||::|       |||     |||||||||||||||||||||||||||
Db     61  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  78

Qy     62  ACAACCCGTCTCTCAAGAGT  81
           ||||||||||||||||||
Db     78  yrAsnProSerLeuLysSer  84

RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
;    APPLICANT: EDELMAN, LENA
;    APPLICANT: MARGARITTE, CHRISTEL
;    APPLICANT: KACZOREK, MICHEL
;    APPLICANT: CHAABIHI, HASSAN
;    TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES: 25
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;       ADDRESSEE: P.C.
;       STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;       CITY: ARLINGTON
```

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STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/793,450
  FILING DATE: 03-MAR-1997
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: FR 94/10566
  FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
  NAME: OBLON, NORMAN F.
  REGISTRATION NUMBER: 24,618
  REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 703-413-3000
  TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 472 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-793-450-8
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Alignment Scores:
Pred. No.:              6.98e-05        Length:         472
Score:                  98.20           Matches:        19
Percent Similarity:     65.62%          Conservative:   2
Best Local Similarity:  59.38%          Mismatches:     3
Query Match:            70.14%          Indels:         8
DB:                                     Gaps:           0

DELETED2 (1-81) x US-08-793-450-8 (1-472)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
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Db   61 GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78

Qy   62 ACAACCGTCTCTCAAGAGT 81
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Db   78 yrAsnProSerLeuLysSer 84
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RESULT 5
US-09-372-425A-6
; Sequence 6, Application US/09372425A
; Patent No. 6475749
GENERAL INFORMATION:
  APPLICANT: Sherie L. Morrison
  APPLICANT: Ramon Montano
  TITLE OF INVENTION: Improved Rh Antibody
  NUMBER OF SEQUENCES: 11
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
    STREET: 2029 Century Park East, Suite 3800
    CITY: Los Angeles
    STATE: CA
    COUNTRY: USA
    ZIP: 90067
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy Disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: Windows 98
    SOFTWARE: MS Word
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/372,425A
    FILING DATE: August 11, 1999
    CLASSIFICATION: 435
```

```
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: Oldenakmp, David J.
  REGISTRATION NUMBER: 29,421
  REFERENCE/DOCKET NUMBER: 510015-223
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (310) 788-5000
  TELEFAX: (310) 788-5100
INFORMATION FOR SEQ ID NO: 6:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 429 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: Heavy chain without Tailpiece - AA
US-09-372-425A-6
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Alignment Scores:
Pred. No.:              0.00033         Length:         429
Score:                  93.20           Matches:        18
Percent Similarity:     65.62%          Conservative:   3
Best Local Similarity:  66.25%          Mismatches:     3
Query Match:            66.57%          Indels:         8
DB:                                     Gaps:           0

DELETED2 (1-81) x US-09-372-425A-6 (1-429)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
        |||::      |||      ::::         ||||||||||||||||||||||||||||
Db   61 GlyLys----GlyLeu---GluTrpIleGlyGluIleAspHisSerGlySerThrAsnT 78

Qy   62 ACAACCGTCTCTCAAGAGT 81
        ||||||||||||||||||
Db   78 yrAsnProSerLeuLysSer 84
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RESULT 6
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 6300064
GENERAL INFORMATION:
  APPLICANT: Knappik, Achim
  APPLICANT: Pack, Peter
  APPLICANT: Ilag, Vic
  APPLICANT: Ge, Liming
  APPLICANT: Moroney, Simon
  APPLICANT: Plueckthun, Andreas
  TITLE OF INVENTION: Protein/(Poly)peptide libraries
  NUMBER OF SEQUENCES: 373
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
    STREET: 1251 Avenue of the Americas
    CITY: New York
    STATE: New York
    COUNTRY: USA
    ZIP: 10021
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/025,769B
    FILING DATE: 18-FEB-1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: EP 95 11 3021.0
    FILING DATE: 18-AUG-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: James F. Haley, Jr., Esq.
    REGISTRATION NUMBER: 27,794
    REFERENCE/DOCKET NUMBER: MORPHO/5
  TELECOMMUNICATION INFORMATION:
```

```
;               TELEPHONE:    (212)596-9000
;               TELEFAX:      (212)596-9090
;       INFORMATION FOR SEQ ID NO: 25:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 118 amino acids
;               TYPE: amino acid
;               STRANDEDNESS:
;               TOPOLOGY: linear
;               MOLECULE TYPE: protein
US-09-025-769B-25

Alignment Scores:
Pred. No.:              0.000291          Length:           118
Score:                  92.10             Matches:           21
Percent Similarity:     50.00%            Conservative:       1
Best Local Similarity:  47.73%            Mismatches:         3
Query Match:            65.79%            Indels:            19
DB:                                       Gaps:               1

DELETED2 (1-81) x US-09-025-769B-25 (1-118)

Qy    3 GGCGAGTCAGGAGATATTAGCAGC---------------------------- 24
          |||  |||   ||||||||
Db   26 GlyGlySer----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl 44

Qy   25 ----TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAA 77
              ||||:::  ||||| |||||||||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
        ||||
Db   64 sSer 65

RESULT 7
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
   GENERAL INFORMATION:
       APPLICANT: Knappik, Achim
                  Pack, Peter
                  Ilag, Vic
                  Ge, Liming
                  Moroney, Simon
                  Plueckthun, Andreas
   TITLE OF INVENTION: Protein/(Poly)peptide libraries
   NUMBER OF SEQUENCES: 373
   CORRESPONDENCE ADDRESS:
       ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
                  White & McAuliffe
       STREET: 1666 K Street, N.W., Suite 300
       CITY: Washington
       STATE: D.C.
       COUNTRY: USA
       ZIP: 20006
   COMPUTER READABLE FORM:
       MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible
       OPERATING SYSTEM: PC-DOS/MS-DOS
       SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
   CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/09/490,070A
       FILING DATE: 24-Jan-2000
   PRIOR APPLICATION DATA:
       APPLICATION NUMBER: EP 95 11 3021.0
       FILING DATE: 18-AUG-1995
   ATTORNEY/AGENT INFORMATION:
       NAME: Colin G. Sandercock, Esq.
       REGISTRATION NUMBER: 31,298
       REFERENCE/DOCKET NUMBER: 37629-0005
   TELECOMMUNICATION INFORMATION:
       TELEPHONE: (202) 912-2000
       TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 25:
```

```
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 118 amino acids
;               TYPE: amino acid
;               STRANDEDNESS: <Unknown>
;               TOPOLOGY: linear
;               MOLECULE TYPE: protein
;               SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Alignment Scores:
Pred. No.:              0.000291          Length:           118
Score:                  92.10             Matches:           21
Percent Similarity:     50.00%            Conservative:       1
Best Local Similarity:  47.73%            Mismatches:         3
Query Match:            65.79%            Indels:            19
DB:                                       Gaps:               1

DELETED2 (1-81) x US-09-490-070A-25 (1-118)

Qy    3 GGCGAGTCAGGAGATATTAGCAGC---------------------------- 24
          |||  |||   ||||||||
Db   26 GlyGlySer----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl 44

Qy   25 ----TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAA 77
              ||||:::  ||||| |||||||||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
        ||||
Db   64 sSer 65

RESULT 8
US-09-490-153-25
; Sequence 25, Application US/0490153
; Patent No. 6706484
   GENERAL INFORMATION:
       APPLICANT: Knappik, Achim
                  Pack, Peter
                  Ilag, Vic
                  Ge, Liming
                  Moroney, Simon
                  Plueckthun, Andreas
   TITLE OF INVENTION: Protein/(Poly)peptide libraries
   NUMBER OF SEQUENCES: 373
   CORRESPONDENCE ADDRESS:
       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
       STREET: 1251 Avenue of the Americas
       CITY: New York
       STATE: New York
       COUNTRY: USA
       ZIP: 10021
   COMPUTER READABLE FORM:
       MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible
       OPERATING SYSTEM: PC-DOS/MS-DOS
       SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
   CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/09/490,153
       FILING DATE: 24-Jan-2000
   PRIOR APPLICATION DATA:
       APPLICATION NUMBER: US/09/025,769B
       FILING DATE: 18-FEB-1998
       APPLICATION NUMBER: EP 95 11 3021.0
       FILING DATE: 18-AUG-1995
   ATTORNEY/AGENT INFORMATION:
       NAME: James F. Haley, Jr., Esq.
       REGISTRATION NUMBER: 27,794
       REFERENCE/DOCKET NUMBER: MORPHO/5
   TELECOMMUNICATION INFORMATION:
       TELEPHONE: (212)596-9000
       TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
   SEQUENCE CHARACTERISTICS:
```

```
;          LENGTH: 118 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: <Unknown>
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Alignment Scores:
Pred. NO.:             0.000291      Length:        118
Score:                 92.10         Matches:        21
Percent Similarity:    50.00%        Conservative:    1
Best Local Similarity: 47.73%        Mismatches:      3
Query Match:           65.79%        Indels:         19
DB:                                  Gaps:            1

DELETED2 (1-81) x US-09-490-153-25 (1-118)

Qy    3 GGCGAGTCAGGATATTAGCAGC------------------------------------- 24
          |||  |||  ||||||||
Db   26 GlyGlySer----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl 44

Qy   25 ------TGGTTAGCCGAAATCAATCATCATGTGGAAGCACCAACTACAACCCGTCTCTCAA 77
          ||:::  |||||    |||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
          |||
Db   64 sSer 65

RESULT 9
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;              Pack, Peter
;              Ilag, Vic
;              Ge, Liming
;              Moroney, Simon
;              Plueckthun, Andreas
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;     ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
;     STREET: 1251 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10021
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/490,324
;     FILING DATE: 24-Jan-2000
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/025,769
;     FILING DATE: 18-FEB-1998
;     APPLICATION NUMBER: EP 95 11 3021.0
;     FILING DATE: 18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: James F. Haley, Jr., Esq.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: MORPHO/5
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212)596-9000
;     TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 118 amino acids
```

```
;          TYPE: amino acid
;          STRANDEDNESS: <Unknown>
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Alignment Scores:
Pred. No.:             0.000291      Length:        118
Score:                 92.10         Matches:        21
Percent Similarity:    50.00%        Conservative:    1
Best Local Similarity: 47.73%        Mismatches:      3
Query Match:           65.79%        Indels:         19
DB:                                  Gaps:            1

DELETED2 (1-81) x US-09-490-324-25 (1-118)

Qy    3 GGCGAGTCAGGATATTAGCAGC------------------------------------- 24
          |||  |||  ||||||||
Db   26 GlyGlySer----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGl 44

Qy   25 ------TGGTTAGCCGAAATCAATCATCATGTGGAAGCACCAACTACAACCCGTCTCTCAA 77
          ||:::  |||||    |||||||||||||||||||||
Db   44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
          |||
Db   64 sSer 65

RESULT 10
US-08-545-809A-137
; Sequence 137, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT: Honjo, Tasuku
;   APPLICANT: Matsuda, Fumihiko
;   TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES: 145
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson, P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: US
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: Windows95
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/545,809A
;     FILING DATE: 27-MAR-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/JP93/00603
;     FILING DATE: 10-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Freeman, John W.
;     REGISTRATION NUMBER: 29,066
;     REFERENCE/DOCKET NUMBER: 06501/004001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-542-5070
;     TELEFAX: 617-542-8906
;     TELEX: 200154
; INFORMATION FOR SEQ ID NO: 137:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 120 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-545-809A-137
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```
Alignment Scores:
Pred. No.:              0.000402        Length:                 120
Score:                  91.10           Matches:                20
Percent Similarity:     52.27%          Conservative:           3
Best Local Similarity:  45.45%          Mismatches:             2
Query Match:            65.07%          Indels:                 19
DB:                                     Gaps:                   1

DELETED2 (1-81) x US-08-545-809A-137 (1-120)

Qy   3  GGCGAGTCAGGATATTAGCAGC------------------------------------ 24
        |||::|:|||   ||||||
Db  45  GlyAspSer----IleSerSerGlyAsnTrpIleTrpValArgGlnProProGlyLysGl 63

Qy  25  ------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAA 77
        ||:::    ||||:||||:|||||||||||||||||||||
Db  63  yLeuGluTrpIleGlyGluIleHisHisSerGlySerThrTyrTyrTyrAsnProSerLeuLy 83

Qy  78  GAGT   81
        ||||
Db  83  sSer   84

RESULT 11
US-09-471-276-835
; Sequence 835, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 835
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -26..-1
US-09-471-276-835

Alignment Scores:
Pred. No.:              0.0015          Length:                 147
Score:                  87.20           Matches:                16
Percent Similarity:     65.62%          Conservative:           5
Best Local Similarity:  50.00%          Mismatches:             3
Query Match:            62.29%          Indels:                 8
DB:                                     Gaps:                   0

DELETED2 (1-81) x US-09-471-276-835 (1-147)

Qy   2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
        ||      |||::|  |||::||||||
Db  69  GlyLys----GlyLeu----GluTrpIleSerGluIleAspHisGlyGlyAsnThrAsnT 86

Qy  62  ACAACCCGTCTCTCAAGAGT 81
        ||||||||||||
Db  86  yrAsnProSerLeuLysSer 92

RESULT 12
US-08-466-151-5
; Sequence 5, Application US/08466151
```

```
Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERNCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9981
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.:              0.0019          Length:                 130
Score:                  86.30           Matches:                17
Percent Similarity:     40.74%          Conservative:           5
Best Local Similarity:  31.48%          Mismatches:             27
Query Match:            61.64%          Indels:                 1
DB:                                     Gaps:                   1

DELETED2 (1-81) x US-08-466-151-5 (1-130)

Qy   1  CGGGCGAGTCAGGATATTAGC----------------------------------- 21
        :::   ||||||  :||||
Db  13  LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32

Qy  22  -----------------------------------AGCTGGTTAGCCGAAATC 39
                                           ||:::
Db  33  AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy  40  AATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT 81
        ||||||||::||||||||||||||||||||||
Db  53  AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 13
```

US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.:   0.0019
Score: 86.30
Percent Similarity: 40.74%
Best Local Similarity: 31.48%
Query Match: 61.64%
DB: 3

Length: 130
Matches: 17
Conservative: 5
Mismatches: 5
Indels: 27
Gaps: 1

DELETED2 (1-81) x US-08-466-163B-5 (1-130)

```
Qy    1 CGGGCGAGTCAGGATATTAGC---------------------------------- 21
          ::: |||||| :::|||
Db   13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32

Qy   22 ------------------------------------------AGCTGGTTAGCCGAAATC 39
                                                    |||:::||
Db   33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy   40 AATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT 81
         ||||||||||||::||||:::|||:::|||||||||||||||
Db   53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66
```

RESULT 14
US-09-802-096-5
; Sequence 5, Application US/0980209 6
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-802-096-5

Alignment Scores:
Pred. No.:   0.0019
Score: 86.30
Percent Similarity: 40.74%
Best Local Similarity: 31.48%
Query Match: 61.64%
DB: 4

Length: 130
Matches: 17
Conservative: 5
Mismatches: 5
Indels: 27
Gaps: 1

DELETED2 (1-81) x US-09-802-096-5 (1-130)

```
Qy    1 CGGGCGAGTCAGGATATTAGC---------------------------------- 21
          ::: |||||| :::|||
Db   13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32

Qy   22 ------------------------------------------AGCTGGTTAGCCGAAATC 39
                                                    |||:::||
Db   33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy   40 AATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT 81
         ||||||||||||::||||:::|||:::|||||||||||||||
Db   53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66
```

RESULT 15
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Alignment Scores:
Pred. No.:   0.0019
Score: 86.30
Percent Similarity: 40.74%
Best Local Similarity: 31.48%
Query Match: 61.64%
DB: 4

Length: 130
Matches: 17
Conservative: 5
Mismatches: 5
Indels: 27
Gaps: 1

DELETED2 (1-81) x US-09-802-077-5 (1-130)

```
Qy    1 CGGGCGAGTCAGGATATTAGC---------------------------------- 21
          ::: |||||| :::|||
Db   13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32

Qy   22 ------------------------------------------AGCTGGTTAGCCGAAATC 39
                                                    |||:::||
Db   33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52

Qy   40 AATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT 81
         ||||||||||||::||||:::|||:::|||||||||||||||
Db   53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66
```

OM nucleic - protein search, using frame_plus_n2p model

Copyright   GenCore version 5.1.6
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Run on: August 4, 2005, 20:04:58 ; Search time 105.5 Seconds
(without alignments)
599.473 Million cell updates/sec

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Perfect score: 140
Sequence: 1 CGGGCGAGTCAGGATATTAG.........ACAACCCGTCTCTCAAGAGT 81

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Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop   6.0 , Delext   0.1

Searched: 1752860 seqs, 390397842 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=NOLAN463-3B @CGN_1_1.199 @runat_04082005_120456_19700
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1
-FGAPOP=6 -FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	100.1	71.5	253	10	US-09-880-748-1333	Sequence 1333, Ap
2	100.1	71.5	253	15	US-10-293-418-1333	Sequence 1333, Ap
3	99.9	71.4	125	15	US-10-371-942-118	Sequence 118, App
4	98.2	70.1	80	14	US-10-078-958-2	Sequence 2, Appli
5	98.2	70.1	97	14	US-10-194-975-40	Sequence 40, Appl
6	98.2	70.1	97	15	US-10-308-817-83	Sequence 83, Appl
7	98.2	70.1	97	15	US-10-032-037B-87	Sequence 87, Appl
8	98.2	70.1	97	15	US-10-029-988B-87	Sequence 87, Appl
9	98.2	70.1	97	15	US-10-032-423A-87	Sequence 87, Appl
10	98.2	70.1	97	15	US-10-453-698-83	Sequence 83, Appl
11	98.2	70.1	97	15	US-10-029-926B-87	Sequence 87, Appl
12	98.2	70.1	97	16	US-10-379-392-47	Sequence 47, Appl
13	98.2	70.1	114	17	US-10-733-532-128	Sequence 128, App
14	98.2	70.1	115	17	US-10-898-408-12	Sequence 12, Appl
15	98.2	70.1	117	9	US-09-864-761-44315	Sequence 44315, A
16	98.2	70.1	118	15	US-10-371-942-90	Sequence 90, Appl
17	98.2	70.1	118	17	US-10-893-576-192	Sequence 192, App
18	98.2	70.1	122	15	US-10-360-828-63	Sequence 63, Appl
19	98.2	70.1	125	15	US-10-371-942-110	Sequence 110, App
20	98.2	70.1	139	14	US-10-300-675-2	Sequence 2, Appli
21	98.2	70.1	139	17	US-10-910-124-2	Sequence 2, Appli
22	98.2	70.1	139	17	US-10-893-576-43	Sequence 43, Appl
23	98.2	70.1	142	17	US-10-484-790A-10	Sequence 10, Appl
24	98.2	70.1	223	10	US-09-972-655-66	Sequence 66, Appl
25	98.2	70.1	229	10	US-09-972-655-82	Sequence 82, Appl
26	98.2	70.1	230	10	US-09-972-656-72	Sequence 72, Appl
27	98.2	70.1	249	10	US-09-880-748-1321	Sequence 1321, Ap
28	98.2	70.1	249	15	US-10-293-418-1321	Sequence 1321, Ap
29	98.2	70.1	250	10	US-09-880-748-1413	Sequence 1413, Ap
30	98.2	70.1	250	15	US-10-293-418-1413	Sequence 1413, Ap
31	98.2	70.1	254	10	US-09-880-748-1659	Sequence 1659, Ap
32	98.2	70.1	254	15	US-10-293-418-1659	Sequence 1659, Ap
33	98.2	70.1	450	17	US-10-484-790A-17	Sequence 17, Appl
34	98.2	70.1	453	17	US-10-484-790A-18	Sequence 18, Appl
35	97.2	69.4	249	10	US-09-880-748-957	Sequence 957, App
36	97.2	69.4	249	15	US-10-293-418-957	Sequence 957, App
37	95	67.9	246	10	US-09-880-748-1847	Sequence 1847, Ap
38	95	67.9	246	15	US-10-293-418-1847	Sequence 1847, Ap
39	94.2	67.3	123	14	US-10-269-805-31	Sequence 31, Appl
40	94.2	67.3	123	14	US-10-269-805-55	Sequence 55, Appl
41	94.2	67.3	255	10	US-09-880-748-1642	Sequence 1642, Ap
42	94.2	67.3	255	15	US-10-293-418-1642	Sequence 1642, Ap
43	93.7	66.9	116	15	US-10-308-817-189	Sequence 189, App
44	93.7	66.9	116	15	US-10-453-698-189	Sequence 189, App
45	93.2	66.6	250	10	US-09-880-748-993	Sequence 993, App

ALIGNMENTS

RESULT 1
US-09-880-748-1333
; Sequence 1333, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben et al.
;   TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;   FILE REFERENCE: PF523
;   CURRENT APPLICATION NUMBER: US/09/880,748
;   CURRENT FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/212,210
;   PRIOR FILING DATE: 2000-06-15
;   PRIOR APPLICATION NUMBER: 60/240,816
;   PRIOR FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/276,248
;   PRIOR FILING DATE: 2000-10-17
;   PRIOR APPLICATION NUMBER: 60/293,499
;   PRIOR FILING DATE: 2001-05-25

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;   NUMBER OF SEQ ID NOS: 3239
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 1333
;     LENGTH: 253
;     TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1333

Alignment Scores:
Pred. No.:                  0.000755          Length:          253
Score:                      100.10            Matches:         21
Percent Similarity:         50.00%            Conservative:    1
Best Local Similarity:      47.73%            Mismatches:      3
Query Match:                71.50%            Indels:          19
DB:                                           Gaps:            1

DELETED2 (1-81) x US-09-880-748-1333 (1-253)

Qy     3 GGGGAGTCA----------------------------------------GGATAT 17
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Db    26 GlyGluSerPheSerGlyTyrTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy    18 TAGCAGCTGGTTAGCCGAAATCAATCATCAGTCGAAGCACCAACTACAACCCGTCTCTCAA 77
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Db    46 ---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy    78 GAGT 81
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Db    64 sSer 65

RESULT 2
US-10-293-418-1333
;   Sequence 1333, Application US/10293418
;   Publication No. US20030223996A1
;   GENERAL INFORMATION:
;     APPLICANT: Ruben et al.
;     TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;     FILE REFERENCE: PF523P2
;   CURRENT APPLICATION NUMBER: US/10/293,418
;   CURRENT FILING DATE:  2002-11-27
;   PRIOR APPLICATION NUMBER: 60/331,469
;   PRIOR FILING DATE:  2001-11-16
;   PRIOR APPLICATION NUMBER: 60/340,817
;   PRIOR FILING DATE:  2001-12-19
;   PRIOR APPLICATION NUMBER: 09/880,748
;   PRIOR FILING DATE:  2001-06-15
;   PRIOR APPLICATION NUMBER: 60/293,499
;   PRIOR FILING DATE:  2001-05-25
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE:  2001-03-21
;   PRIOR APPLICATION NUMBER: 60/276,248
;   PRIOR FILING DATE:  2001-03-16
;   PRIOR APPLICATION NUMBER: 60/240,816
;   PRIOR FILING DATE:  2000-10-17
;   PRIOR APPLICATION NUMBER: 60/212,210
;   PRIOR FILING DATE:  2000-06-16
;   NUMBER OF SEQ ID NOS: 3247
;   SEQ ID NO 1333
;     LENGTH: 253
;     TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-1333

Alignment Scores:
Pred. No.:                  0.000755          Length:          253
Score:                      100.10            Matches:         21
Percent Similarity:         50.00%            Conservative:    1
Best Local Similarity:      47.73%            Mismatches:      3
Query Match:                71.50%            Indels:          19
DB:                                           Gaps:            1

DELETED2 (1-81) x US-10-293-418-1333 (1-253)
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Qy     3 GGGGAGTCA----------------------------------------GGATAT 17
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Db    26 GlyGluSerPheSerGlyTyrTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy    18 TAGCAGCTGGTTAGCCGAAATCAATCATCAGTCGAAGCACCAACTACAACCCGTCTCTCAA 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    46 ---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy    78 GAGT 81
           ||||
Db    64 sSer 65

RESULT 3
US-10-371-942-118
;   Sequence 118, Application US/10371942
;   Publication No. US20030223994A1
;   GENERAL INFORMATION:
;     APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
;     APPLICANT: Reiter, Yoram
;     TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
;     FILE REFERENCE: 10280-034001
;   CURRENT APPLICATION NUMBER: US/10/371,942
;   CURRENT FILING DATE:  2003-02-20
;   PRIOR APPLICATION NUMBER: US 60/358,994
;   PRIOR FILING DATE:  2002-02-20
;   NUMBER OF SEQ ID NOS: 121
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 118
;     LENGTH: 125
;     TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-371-942-118

Alignment Scores:
Pred. No.:                  0.000704          Length:          125
Score:                      99.90             Matches:         22
Percent Similarity:         50.00%            Conservative:    1
Best Local Similarity:      47.83%            Mismatches:      2
Query Match:                71.36%            Indels:          21
DB:                                           Gaps:            1

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Qy     3 GGGGAGTCAGGAGATATTAGCAGC-------------------------- 24
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Db    26 GlyGlySer------IleSerSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44

Qy    25 --------------TGGTTAGCCGAAATCAATCATCAGTCGAAGCACCACCACCACCCGTC 71
                         ||:::  |||||||||||||||||||||||||||||||||||
Db    44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64

Qy    72 TCTCAAGAGT 81
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Db    64 rLeuLysSer 67

RESULT 4
US-10-078-958-2
;   Sequence 2, Application US/10078958
;   Publication No. US20030070185A1
;   GENERAL INFORMATION:
;     APPLICANT: JAKOBOVITS, AYA
;     APPLICANT: KUCHERLAPATI, RAJU
;     APPLICANT: KLAPHOLZ, SUSAN
;     APPLICANT: MENDEZ, MICHAEL J.
;     APPLICANT: GREEN, LARRY
;     TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;     TITLE OF INVENTION: PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;     TITLE OF INVENTION: THEREFROM
;     FILE REFERENCE: CELL 4.18 CON
;   CURRENT APPLICATION NUMBER: US/10/078,958
;   CURRENT FILING DATE:  2002-02-19
;   PRIOR APPLICATION NUMBER: 08/759,620
;   PRIOR FILING DATE:  1996-12-03
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; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2

Alignment Scores:
Pred. No.:              0.00107      Length:       80
Score:                  98.20        Matches:      19
Percent Similarity:     65.62%       Conservative: 2
Best Local Similarity:  59.38%       Mismatches:   3
Query Match:            70.14%       Indels:       8
DB:                     14           Gaps:         0

DELETED2 (1-81) x US-10-078-958-2 (1-80)

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Db   25 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 42

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||||||||
Db   42 yrAsnProSerLeuLysSer 48

RESULT 5
US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40

Alignment Scores:
Pred. No.:              0.00111      Length:       97
Score:                  98.20        Matches:      19
Percent Similarity:     65.62%       Conservative: 2
Best Local Similarity:  59.38%       Mismatches:   3
Query Match:            70.14%       Indels:       8
DB:                     14           Gaps:         0

DELETED2 (1-81) x US-10-194-975-40 (1-97)

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Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 6
US-10-308-817-83
; Sequence 83, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
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; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-308-817-83

Alignment Scores:
Pred. No.:              0.00111      Length:       97
Score:                  98.20        Matches:      19
Percent Similarity:     65.62%       Conservative: 2
Best Local Similarity:  59.38%       Mismatches:   3
Query Match:            70.14%       Indels:       8
DB:                     15           Gaps:         0

DELETED2 (1-81) x US-10-308-817-83 (1-97)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
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Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 7
US-10-032-037B-87
; Sequence 87, Application US/10032037B
; Publication No. US2004000182 2A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-87

Alignment Scores:
Pred. No.:              0.00111      Length:       97
Score:                  98.20        Matches:      19
Percent Similarity:     65.62%       Conservative: 2
Best Local Similarity:  59.38%       Mismatches:   3
Query Match:            70.14%       Indels:       8
DB:                     15           Gaps:         0

DELETED2 (1-81) x US-10-032-037B-87 (1-97)

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Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 8
US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US2004000183 9A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
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RESULT 12
US-10-379-392-47
; Sequence 47, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
;   APPLICANT: Lazar, Gregory Alan
;   APPLICANT: Desjarlais, John Rudolf
;   APPLICANT: Marshall, Shannon Alicia
;   APPLICANT: Dahiyat, Bassil I.
;   TITLE OF INVENTION: ANTIBODY OPTIMIZATION
;   FILE REFERENCE: A-71386-3 463077-236
;   CURRENT APPLICATION NUMBER: US/10/379,392
;   CURRENT FILING DATE: 2003-03-03
;   PRIOR APPLICATION NUMBER: US 60/360,843
;   PRIOR FILING DATE: 2002-03-01
;   PRIOR APPLICATION NUMBER: US 60/384,197
;   PRIOR FILING DATE: 2002-05-29
;   NUMBER OF SEQ ID NOS: 184
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-379-392-47

Alignment Scores:
Pred. No.:   0.00111   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 16   Gaps: 0

DELETED2 (1-81) x US-10-379-392-47 (1-97)

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           ||::: || |||::: ||||||||||||||||||||||||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGlulleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
           ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 13
US-10-733-532-128
; Sequence 128, Application US/10733532
; Publication No. US20050026246A1
; GENERAL INFORMATION:
;   APPLICANT: Sale, Julian E.
;   APPLICANT: Neuberger, Michael S.
;   APPLICANT: Cumbers, Sarah J.
;   TITLE OF INVENTION: Method of Generating Diversity
;   FILE REFERENCE: 18396/2002B
;   CURRENT APPLICATION NUMBER: US/10/733,532
;   CURRENT FILING DATE: 2003-12-11
;   PRIOR APPLICATION NUMBER: PCT/GB02/02688
;   PRIOR FILING DATE: 2002-06-11
;   PRIOR APPLICATION NUMBER: 10/146,505
;   PRIOR FILING DATE: 2002-05-15
;   PRIOR APPLICATION NUMBER: 09/879,813
;   PRIOR FILING DATE: 2001-06-11
;   NUMBER OF SEQ ID NOS: 130
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-733-532-128

Alignment Scores:
Pred. No.:   0.00115   Length: 114
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2

Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 17   Gaps: 0

DELETED2 (1-81) x US-10-733-532-128 (1-114)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
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Db   36 GlyLys---GlyLeu---GluTrpIleGlyGlulleAsnHisSerGlySerThrAsnT 53

Qy   62 ACAACCCGTCTCTCAAGAGT 81
           ||||||||||||||||
Db   53 yrAsnProSerLeuLysSer 59

RESULT 14
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
;   APPLICANT: GALIBERT, Laurent J.
;   APPLICANT: YAN, Wei
;   TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
;   FILE REFERENCE: 3467-A
;   CURRENT APPLICATION NUMBER: US/10/898,408
;   CURRENT FILING DATE: 2004-07-23
;   PRIOR APPLICATION NUMBER: 60/490,027
;   PRIOR FILING DATE: 2003-07-25
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.:   0.00115   Length: 115
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: 17   Gaps: 0

DELETED2 (1-81) x US-10-898-408-12 (1-115)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
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Db   42 GlyLys---GlyLeu---GluTrpIleGlyGlulleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
           ||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 15
US-09-864-761-44315
; Sequence 44315, Application US/09864761
; Patent No. US2002004B763A1
; GENERAL INFORMATION:
;   APPLICANT: Penn, Sharron G.
;   APPLICANT: Rank, David R.
;   APPLICANT: Hanzel, David K.
;   APPLICANT: Chen, Wensheng
;   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;   TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;   FILE REFERENCE: Aeomica-X-1
;   CURRENT APPLICATION NUMBER: US/09/864,761
;   CURRENT FILING DATE: 2001-05-23
;   PRIOR APPLICATION NUMBER: US 60/180,312
;   PRIOR FILING DATE: 2000-02-04
;   PRIOR APPLICATION NUMBER: US 60/207,456
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: US 09/632,366
;   PRIOR FILING DATE: 2000-08-03

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;   PRIOR APPLICATION NUMBER: GB 24263.6
;   PRIOR FILING DATE: 2000-10-04
;   PRIOR APPLICATION NUMBER: US 60/236,359
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: PCT/US01/00666
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00667
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00664
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00669
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00665
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00668
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00663
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00662
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00661
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: PCT/US01/00670
;   PRIOR FILING DATE: 2001-01-30
;   PRIOR APPLICATION NUMBER: US 60/234,687
;   PRIOR FILING DATE: 2000-09-21
;   PRIOR APPLICATION NUMBER: US 09/608,408
;   PRIOR FILING DATE: 2000-06-30
;   PRIOR APPLICATION NUMBER: US 09/774,203
;   PRIOR FILING DATE: 2001-01-29
;   NUMBER OF SEQ ID NOS: 49117
;   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;   SEQ ID NO 44315
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AB019439.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.54
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.57
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
;   OTHER INFORMATION: EST_HUMAN HIT: BE672445.1, EVALUE 2.00e-57
;   OTHER INFORMATION: SWISSPROT HIT: P06331, EVALUE 1.00e-53
US-09-864-761-44315

Alignment Scores:
Pred. No.:              0.00115        Length:         117
Score:                  98.20          Matches:        19
Percent Similarity:     65.62%         Conservative:   2
Best Local Similarity:  59.38%         Mismatches:     3
Query Match:            70.14%         Indels:         8
DB:                     9              Gaps:           0

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Db      45 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  62

Qy      62 ACAACCCGTCTCTCAAGAGT  81
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Db      62 yrAsnProSerLeuLysSer  68

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Job time : 106.5 secs
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     August 4, 2005, 19:56:53 ; Search time 341.5 Seconds
                        (without alignments)
                        554.076 Million cell updates/sec

Title:          DELETED2
Perfect score:  140
Sequence:       1 CGGGCGAGTCAGGATATTAG.........ACAACCCGTCTCTCAAGAGT 81

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                Ygapop 10.0 , Ygapext  0.1
                Fgapop  6.0 , Fgapext  0.1
                Delop   6.0 , Delext   0.1

Searched:       6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters:     13918532

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-DB=Pending_Patents_AA_Main -QFMT=fastan -SUFFIX=rapm -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN_1_1_804 @runat_04082005_120455_19651_NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :      Pending_Patents_AA_Main:*
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        3:  /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
        4:  /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
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        7:  /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
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       13:  /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
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       16:  /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
       17:  /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
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       19:  /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
       20:  /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
       21:  /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
       22:  /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
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       26:  /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
       27:  /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
       28:  /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
       29:  /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
       30:  /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
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       32:  /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
       33:  /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
       34:  /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
       35:  /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
       36:  /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104.4	74.6	124	22	US-09-791-537-89288	Sequence 89288, A
2	102.1	72.9	125	22	US-09-791-537-111128	Sequence 111128,
3	101.7	72.6	87	22	US-09-791-537-144795	Sequence 144795,
4	101.7	72.6	125	22	US-09-791-537-111072	Sequence 111072,
5	101.6	72.6	119	22	US-09-791-537-716	Sequence 716, App
6	101.6	71.7	143	22	US-09-791-537-36503	Sequence 36503, A
7	100.4	71.6	97	22	US-09-791-537-78283	Sequence 78283, A
8	100.2	71.6	105	22	US-09-791-537-22691	Sequence 22691, A
9	100.1	71.5	253	1	PCT-US01-19110-1333	Sequence 1333, Ap
10	100.1	71.5	253	23	US-09-880-748-1333	Sequence 1333, Ap
11	100.1	71.5	253	1	US-10-293-418-1333	Sequence 1333, Ap
12	99.9	71.4	121	22	US-09-791-537-110576	Sequence 110576,
13	99.9	71.4	125	1	PCT-US03-05128-118	Sequence 118, App
14	99.9	71.4	125	29	US-10-371-942-118	Sequence 118, App
15	98.7	70.5	119	22	US-09-791-537-110532	Sequence 110532,
16	98.2	70.5	130	22	US-09-791-537-68863	Sequence 68863, A
17	98.2	70.1	67	22	US-09-791-537-122614	Sequence 122614,
18	98.2	70.1	73	22	US-09-791-537-134695	Sequence 134695,
19	98.2	70.1	80	26	US-10-078-958-2	Sequence 2, Appli
20	98.2	70.1	88	22	US-09-791-537-111396	Sequence 111396,
21	98.2	70.1	90	22	US-09-791-537-130857	Sequence 130857,
22	98.2	70.1	91	22	US-09-791-537-130896	Sequence 130896,
23	98.2	70.1	92	22	US-09-791-537-130953	Sequence 130953,
24	98.2	70.1	92	22	US-09-791-537-130969	Sequence 130969,
25	98.2	70.1	93	22	US-09-791-537-151700	Sequence 151700,
26	98.2	70.1	93	22	US-09-791-537-152140	Sequence 152140,
27	98.2	70.1	96	22	US-09-791-537-152186	Sequence 152186,
28	98.2	70.1	97	1	PCT-US02-22011-40	Sequence 40, Appl
29	98.2	70.1	97	1	PCT-US02-38450-83	Sequence 83, Appl
30	98.2	70.1	97	1	PCT-US03-06598-47	Sequence 47, Appl
31	98.2	70.1	97	12	US-08-896-535-76	Sequence 76, Appl
32	98.2	70.1	97	19	US-09-508-110-69	Sequence 69, Appl
33	98.2	70.1	97	22	US-09-751-181-87	Sequence 87, Appl
34	98.2	70.1	97	22	US-09-791-537-78284	Sequence 78284, A
35	98.2	70.1	97	22	US-09-791-537-80274	Sequence 80274, A
36	98.2	70.1	97	22	US-09-791-537-11367	Sequence 111367,
37	98.2	70.1	97	22	US-09-791-537-126333	Sequence 126333,
38	98.2	70.1	97	22	US-09-791-537-130951	Sequence 130951,
39	98.2	70.1	97	26	US-10-029-9268-87	Sequence 87, Appl
40	98.2	70.1	97	26	US-10-029-988B-87	Sequence 87, Appl
41	98.2	70.1	97	26	US-10-032-037B-87	Sequence 87, Appl
42	98.2	70.1	97	26	US-10-032-423A-87	Sequence 87, Appl
43	98.2	70.1	97	27	US-10-189-258A-87	Sequence 87, Appl
44	98.2	70.1	97	27	US-10-194-975-40	Sequence 40, Appl

ALIGNMENTS

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RESULT 1
US-09-791-537-89288
; Sequence 89288, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
```

```
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION:  THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 89288
;    LENGTH: 124
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-89288

Alignment Scores:
Pred. No.:                  0.000343          Length:            124
Score:                      104.40            Matches:           20
Percent Similarity:         45.28%            Conservative:      4
Best Local Similarity:      37.74%            Mismatches:        3
Query Match:                74.57%            Indels:            26
DB:                         22                Gaps:              1

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Db        13  LysLeuSerGluAspLeuSerLeuThrCysAlaValTyrGlySerPheSerGlyTyr  32

Qy        22  ------------------------AGCTGGTTAGCCGAAATCAAT  42
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Db        33  TyrTrpSerTrpIleArgArgProGlyLysGlyLeuGlyGluIleGlyGluIleAsn  52

Qy        43  CATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT  81
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Db        53  HisSerGlySerThrAsnTyrAsnProSerLeuLysSer  65


RESULT 2
US-09-791-537-111128
;  Sequence 111128, Application US/09791537
;  GENERAL INFORMATION:
;  APPLICANT:  Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION:  THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 111128
;    LENGTH: 125
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-111128

Alignment Scores:
Pred. No.:                  0.000691          Length:            125
Score:                      102.10            Matches:           21
Percent Similarity:         52.27%            Conservative:      2
Best Local Similarity:      47.73%            Mismatches:        2
Query Match:                72.93%            Indels:            19
DB:                         22                Gaps:              1

DELETED2 (1-81) x US-09-791-537-111128 (1-125)

Qy         3  GGCGAGTCGAGGATATTAGC---------------------------  21
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Db        26  GlyGluSer----ValSerGlyTyrTyrTrpThrTrpIleArgGlnProProGlyLysGl  44

Qy        22  ----AGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAA  77
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Db        44  uProGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuIly  64

Qy        78  GAGT  81
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Db        64  sSer  65


RESULT 3
US-09-791-537-144795
;  Sequence 144795, Application US/09791537
;  GENERAL INFORMATION:
;  APPLICANT:  Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION:  THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 144795
;    LENGTH: 87
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-144795

Alignment Scores:
Pred. No.:                  0.000714          Length:            87
Score:                      101.70            Matches:           21
Percent Similarity:         59.46%            Conservative:      1
Best Local Similarity:      56.76%            Mismatches:        2
Query Match:                72.64%            Indels:            13
DB:                         22                Gaps:              1

DELETED2 (1-81) x US-09-791-537-144795 (1-87)

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              |||||||| ||                                  ||:::
Db         3  SerGlyTyr-SerGlySerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGl  22

Qy        33  CGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT  81
              |||||||||||||||||||||||||||||||||||||||
Db        22  yGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer  38


RESULT 4
US-09-791-537-111072
;  Sequence 111072, Application US/09791537
;  GENERAL INFORMATION:
;  APPLICANT:  Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION:  THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 111072
;    LENGTH: 125
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-111072

Alignment Scores:
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Score:                      101.70            Matches:           21
Percent Similarity:         59.46%            Conservative:      1
Best Local Similarity:      56.76%            Mismatches:        2
Query Match:                72.64%            Indels:            13
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DELETED2 (1-81) x US-09-791-537-111072 (1-125)
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DB: 22   Gaps: 0

DELETED2 (1-81) x US-09-791-537-36503 (1-143)

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Db   59 yrAsnProSerLeuLysSer 65

RESULT 7
US-09-791-537-78283
; Sequence 78283, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: . 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78283
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-78283

Alignment Scores:
Pred. No.:   0.00109   Length: 97
Score: 100.40   Matches: 20
Percent Similarity: 43.40%   Conservative: 3
Best Local Similarity: 37.74%   Mismatches: 4
Query Match: 71.71%   Indels: 26
DB: 22   Gaps: 1

DELETED2 (1-81) x US-09-791-537-78283 (1-97)

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Qy   22 -------------------------------AGCTCGGTTAGCCGAAATCAAT 42
                                          ||:::
Db   33 TyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGlyGluIleAsn 52

Qy   43 CATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGT 81
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Db   53 HisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 8
US-09-791-537-22691
; Sequence 22691, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22691
;   LENGTH: 105
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-22691

Qy   9 TCAGGATATTAGC------------------------------AGCTCGGTTAGC 32
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Db   30 SerGlyTyr-SerTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGl 49

Qy   33 CGAAATCAATCATAGTGGAAGCACCAACTACAACCGTCTCTCAAGAGT 81
         |||||||||||||||||||||||||||||||||||||||||||||
Db   49 yGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 5
US-09-791-537-716
; Sequence 716, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 716
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-716

Alignment Scores:
Pred. No.:   0.000794   Length: 119
Score: 101.60   Matches: 19
Percent Similarity: 71.43%   Conservative: 1
Best Local Similarity: 67.86%   Mismatches: 4
Query Match: 72.57%   Indels: 4
DB: 22   Gaps: 0

DELETED2 (1-81) x US-09-791-537-716 (1-119)

Qy   6 GAGTCAGGATATTAGCAGCTCGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAA 65
         ||| ::: ||:::|||||||||||||||||||||||||||
Db   42 GluLysGlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAs 60

Qy   66 CCCGTCTCTCAAGAGT 81
         ||||||||||||||||
Db   60 nProSerLeuLysSer 65

RESULT 6
US-09-791-537-36503
; Sequence 36503, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36503
;   LENGTH: 143
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-36503

Alignment Scores:
Pred. No.:   0.000831   Length: 143
Score: 101.60   Matches: 19
Percent Similarity: 55.56%   Conservative: 1
Best Local Similarity: 52.78%   Mismatches: 2
Query Match: 72.57%   Indels: 14

```
Alignment Scores:
Pred. No.:                    0.00118          Length:                105
Score:                        100.20           Matches:                19
Percent Similarity:           68.75%           Conservative:            3
Best Local Similarity:        59.38%           Mismatches:              2
Query Match:                  71.57%           Indels:                  8
DB:                                            Gaps:                    0

DELETED2 (1-81) x US-09-791-537-22691 (1-105)

Qy       2 GGGCGAGTCAGGATATTAGCAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
           ||| ||::: ||| ::  |||:::  ||||||||||||||||||||||||||||||||||||||
Db      42 GlyLys---ArgLeu----GluTrpIleGlyIleuAsnHisSerGlySerThrAsnT 59

Qy      62 ACAACCCGTCTCTCAAGAGT 81
           ||||||||||||||||||||
Db      59 yrAsnProSerLeuLysSer 65

RESULT 9
PCT-US01-19110-1333
; Sequence 1333, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1333

Alignment Scores:
Pred. No.:                    0.00151          Length:                253
Score:                        100.10           Matches:                21
Percent Similarity:           50.00%           Conservative:            1
Best Local Similarity:        47.73%           Mismatches:              3
Query Match:                  71.50%           Indels:                 19
DB:                                            Gaps:                    1

DELETED2 (1-81) x PCT-US01-19110-1333 (1-253)

Qy       3 GGCGAGTCA----------------------------------------GGATAT 17
           ||| ||||||
Db      26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy      18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAA 77
           ||:::  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46 ---GluTrpIleGlyIleuAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy      78 GAGT 81
           ||||
Db      64 sSer 65

RESULT 10
PCT-US02-36496-1333
; Sequence 1333, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1333

Alignment Scores:
Pred. No.:                    0.00151          Length:                253
Score:                        100.10           Matches:                21
Percent Similarity:           50.00%           Conservative:            1
Best Local Similarity:        47.73%           Mismatches:              3
Query Match:                  71.50%           Indels:                 19
DB:                                            Gaps:                    1

DELETED2 (1-81) x PCT-US02-36496-1333 (1-253)

Qy       3 GGCGAGTCA----------------------------------------GGATAT 17
           ||| ||||||
Db      26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy      18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACACCCGTCTCTCAA 77
           ||:::  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46 ---GluTrpIleGlyIleuAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy      78 GAGT 81
           ||||
Db      64 sSer 65

RESULT 11
US-09-880-748-1333
; Sequence 1333, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1333

Alignment Scores:
Pred. No.:                    0.00151          Length:                253
Score:                        100.10           Matches:                21
Percent Similarity:           50.00%           Conservative:            1
Best Local Similarity:        47.73%           Mismatches:              3
Query Match:                  71.50%           Indels:                 19
DB:                                            Gaps:                    1

DELETED2 (1-81) x US-09-880-748-1333 (1-253)
```

... APPLICANT AND FAMILY MEMBE

; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 110576
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-110576

Alignment Scores:
Pred. No.:   0.00134   Length: 121
Score: 99.90   Matches: 22
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.83%   Mismatches: 2
Query Match: 71.36%   Indels: 21
DB: 22   Gaps: 1

DELETED2 (1-81) x US-09-791-537-110576 (1-121)

Qy   3 GGCGAGTCAGGAGATATTAGCAGC----------------------- 24
           ||| ||| |||||||
Db   26 GlyGlySer----IleSerSerSerTyrTyrTrpGlyTrpIleArgGlnProProGl 44

Qy   25 ---------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTC 71
                   ||||::: ||||||||||||||||||||||||||||||||||||
Db   44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64

Qy   72 TCTCAAGAGT 81
           ||||||||
Db   64 rLeuLysSer 67

RESULT 14
PCT-US03-05128-118
; Sequence 118, Application PC/TUS0305128
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation, et al
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034WO1
; CURRENT APPLICATION NUMBER: PCT/US03/05128
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/359,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-05128-118

Alignment Scores:
Pred. No.:   0.00135   Length: 125
Score: 99.90   Matches: 22
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.83%   Mismatches: 2
Query Match: 71.36%   Indels: 21
DB: 1   Gaps: 1

DELETED2 (1-81) x PCT-US03-05128-118 (1-125)

Qy   3 GGCGAGTCAGGAGATATTAGCAGC----------------------- 24
           ||| ||| |||||||
Db   26 GlyGlySer----IleSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44

Qy   25 ---------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTC 71
                   ||||::: ||||||||||||||||||||||||||||||||||||
Db   44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64

Qy   3 GGCGAGTCA-----------------------------GGATAT 17
           |||||||| ||
Db   26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy   18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAA 77
           |||::: ||||||||||||||||||||||||||||||||||||||
Db   46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
           ||||
Db   64 sSer 65

RESULT 12
US-10-293-418-1333
; Sequence 1333, Application US/10293418
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1333

Alignment Scores:
Pred. No.:   0.00151   Length: 253
Score: .100.10   Matches: 21
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.73%   Mismatches: 3
Query Match: 71.50%   Indels: 19
DB: 28   Gaps: 1

DELETED2 (1-81) x US-10-293-418-1333 (1-253)

Qy   3 GGCGAGTCA-----------------------------GGATAT 17
           |||||||| ||
Db   26 GlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy   18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAA 77
           |||::: ||||||||||||||||||||||||||||||||||||||
Db   46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy   78 GAGT 81
           ||||
Db   64 sSer 65

RESULT 13
US-09-791-537-110576
; Sequence 110576, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek

Qy   72 TCTCAAGAGT 81
             ||||||||||
Db   64 rLeuLysSer 67

RESULT 15
US-10-371-942-118
; Sequence 118, Application US/10371942
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-118

Alignment Scores:
Pred. No.:   0.00135   Length: 125
Score: 99.90   Matches: 22
Percent Similarity: 50.00%   Conservative: 1
Best Local Similarity: 47.83%   Mismatches: 2
Query Match: 71.36%   Indels: 21
DB: 29   Gaps: 1

DELETED2 (1-81) x US-10-371-942-118 (1-125)

Qy   3 GGCGAGTCAGGATATATTAGCAGC------------------------ 24
            ||| ||| ||||||||
Db   26 GlyGlySer----IleSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44

Qy   25 -------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTC 71
            |||::: ||||||||||||||||||||||||||||||||||||||||||||
Db   44 yLysGlyLeuGluTrpIleGlyIleAsnHisSerGlySerThrAsnTyrAsnProSe 64

Qy   72 TCTCAAGAGT 81
            ||||||||||
Db   64 rLeuLysSer 67

Search completed: August 4, 2005, 20:18:16
Job time : 343.5 secs

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:        August  4, 2005, 19:51:37 ; Search time 25 Seconds
                                  (without alignments)
                                  623.485 Million cell updates/sec

Title:         DELETED2
Perfect score: 140
Sequence:      1 CGGGCGAGTCAGGATATTAG........ACAACCCGTCTCTCAAGAGT 81

Scoring table: BLOSUM62
               Xgapop   10.0 , Xgapext   0.1
               Ygapop   10.0 , Ygapext   0.1
               Fgapop    6.0 , Fgapext   0.1
               Delop     6.0 , Delext    0.1

Searched:      28316 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:       566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     PIR_79:*
               1: _pir1:*
               2: _pir2:*
               3: _pir3:*
               4: _pir4:*

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3B/runat_04082005_120454_19622/app_query.fasta_1.263
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN_1_1_63 @runat_04082005_120454_19622 -LONGLOG
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	101.6	72.6	143	2	B49028	Ig heavy chain V-I
2	100.4	71.7	97	2	S26805	Ig heavy chain V r
3	98.2	70.1	97	2	S26898	Ig heavy chain V r
4	98.2	70.1	97	2	S26806	Ig heavy chain V r
5	98.2	70.1	106	2	S37454	Ig mu chain - huma
6	98.2	70.1	122	2	JL0047	Ig heavy chain V r
7	98.2	70.1	126	2	S47010	Ig heavy chain V4.
8	98.2	70.1	140	2	S78052	Ig heavy chain pre
9	98.2	70.1	140	2	A49045	Ig heavy chain V r
10	98.2	70.1	231	2	B23746	Ig Fab region IV-J
11	98	70.0	133	2	PS0341	Ig heavy chain V-D
12	94.2	67.3	97	2	G34964	Ig heavy chain V-I
13	92	65.7	98	2	S26905	Ig heavy chain V r
14	92	65.7	145	2	S78055	Ig heavy chain pre
15	89.2	63.7	97	2	S14474	Ig heavy chain V r
16	88	62.9	129	2	S44114	Ig heavy chain V r
17	87.2	62.3	146	1	G1HUH2	Ig heavy chain pre
18	86.2	61.6	134	2	S54906	Ig heavy chain V r
19	86	61.4	98	2	S26904	Ig heavy chain V r
20	83.7	59.8	134	2	B24672	Ig heavy chain pre
21	83.2	59.4	114	2	I72667	cold agglutinin FS
22	83	59.3	123	2	S30529	Ig heavy chain V r
23	81.2	58.0	97	2	JH0428	Ig gamma chain V r
24	80.3	57.4	116	2	S38718	Ig heavy chain V r
25	80.1	57.2	98	2	S26902	Ig heavy chain V r
26	80.1	57.2	98	2	S12421	Ig heavy chain V r
27	80.1	57.2	130	2	S31673	Ig heavy chain V r
28	80.1	57.2	140	2	A24770	hypothetical hybri
29	79.9	57.1	127	2	S19668	Ig heavy chain V r
30	79.1	56.5	97	2	S26906	Ig heavy chain V r
31	79.1	56.5	97	2	S12416	Ig heavy chain V r
32	79.1	56.5	105	2	S44125	Ig lambda chain V
33	79.1	56.5	130	2	S31690	Ig heavy chain V r
34	79.1	56.5	140	2	I37782	Ig variable region
35	78.9	56.4	99	2	S12412	Ig heavy chain V r
36	78.3	55.9	106	2	S24464	Ig heavy chain V r
37	78.1	55.8	116	2	B26340	Ig heavy chain pre
38	77.9	55.6	118	2	A26340	Ig heavy chain pre
39	77.6	55.4	109	2	PH1673	Ig heavy chain V r
40	77.2	55.1	97	2	PL0118	Ig heavy chain V-I
41	77.2	55.1	99	2	S26899	Ig heavy chain V r
42	77.2	55.1	130	2	S30534	Ig heavy chain V r
43	77.1	55.1	97	2	S26804	Ig heavy chain V r
44	77.1	55.1	97	2	S26808	Ig heavy chain V r
45	77.1	55.1	116	2	S18557	Ig heavy chain V r

```
                              ALIGNMENTS

RESULT 1
B49028
Ig heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: B49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-143 <TIM>
A;Cross-references: GB:S64473; NID:g236906; PIDN:AAB20012.1; PID:g236907
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblascoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:                8.29e-05      Length:           143
Score:                    101.60        Matches:          19
Percent Similarity:       55.56%        Conservative:     1
Best Local Similarity:    52.78%        Mismatches:       2
Query Match:              72.57%        Indels:           14
DB:                       2             Gaps:             0

DELETED2 (1-81) x B49028 (1-143)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          ||||||                   |||::::   |||||||||||||||||||
Db   44 GlyArg-----------------GluTrpIleGlyLeuIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65
```

RESULT 2
S26805
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000117   Length: 97
Score: 100.40   Matches: 20
Percent Similarity: 43.40%   Conservative: 3
Best Local Similarity: 37.74%   Mismatches: 4
Query Match: 71.71%   Indels: 26
DB: Gaps: 1

DELETED2 (1-81) x S26805 (1-97)

Qy   1 CGGGCGAGTCAGGATATTAGC---------------------------------- 21
           ||| |||||| :::|||
Db   13 LysProSerGlnThrLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32

Qy   22 ----------------------------AGCTGGTTAGCCGAAATCAAT 42
                                       ||:::||
Db   33 TyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGly 52

Qy   43 CATAGTGGAAGCACCACCACTACAACCCGTCTCTCAAGAGT 81
           ||||||||||||||||||||||||
Db   53 HisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 3
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898; S12420
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12420
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <SAN>
A;Cross-references: EMBL:X56364
A;Experimental source: V(H)4.2
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000228   Length: 97

Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: Gaps: 0

DELETED2 (1-81) x S26898 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
           ||||:|| ||| ||| :::: ||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
           ||||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 4
S26806
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26806
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur.J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000228   Length: 97
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: Gaps: 0

DELETED2 (1-81) x S26806 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
           ||||:|| ||| ||| :::: ||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
           ||||||||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 5
S37454
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A;Reference number: S37453
A;Accession: S37454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MCI>
A;Cross-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Alignment Scores:
Pred. No.:   0.000229   Length: 106

```
Score:                    98.20        Matches:        19
Percent Similarity:       65.62%       Conservative:    2
Best Local Similarity:    59.38%       Mismatches:      3
Query Match:              70.14%       Indels:          8
DB:                                    Gaps:            0

DELETED2 (1-81) x S37454 (1-106)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
        |||::::  |||     ||||||||||||||||||||||||||
Db   20 GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 37

Qy   62 ACAACCCGTCTCTCAAGAGT 81
        |||||||||||||||
Db   37 yrAsnProSerLeuLysSer 43
```

RESULT 6
JL0047
Ig heavy chain V region precursor (clone cR18) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: JL0047
R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5
submitted to the EMBL Data Library, July 1988
A;Reference number: JL0047; MUID:88258392; PMID:3313445
A;Accession: JL0047
A;Molecule type: mRNA
A;Residues: 1-122 <BAE>
A;Experimental source: T-cell line RPMI 8402
A;Note: the authors translated the reading frame which extends to the stop codon; the se
A;Note: this sequence belongs to the VH II subgroup
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-105/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:                0.00023
Score:                    98.20        Length:         122
Percent Similarity:       65.62%       Matches:        19
Best Local Similarity:    59.38%       Conservative:    2
Query Match:              70.14%       Mismatches:      3
DB:                                    Indels:          8
                                       Gaps:            0

DELETED2 (1-81) x JL0047 (1-122)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
        |||::::  |||     ||||||||||||||||||||||||||||
Db   50 GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 67

Qy   62 ACAACCCGTCTCTCAAGAGT 81
        |||||||||||||||
Db   67 yrAsnProSerLeuLysSer 73
```

RESULT 7
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S47010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A;Reference number: S47009
A;Accession: S47010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:                0.00023
Score:                    98.20        Length:         126
Percent Similarity:       65.62%       Matches:        19
Best Local Similarity:    59.38%       Conservative:    2
Query Match:              70.14%       Mismatches:      3
DB:                                    Indels:          8
                                       Gaps:            0

DELETED2 (1-81) x S47010 (1-126)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
        |||::::  |||     ||||||||||||||||||||||||||||
Db   42 GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
        |||||||||||||||
Db   59 yrAsnProSerLeuLysSer 65
```

RESULT 8
S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and l
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>

```
Alignment Scores:
Pred. No.:                0.000231
Score:                    98.20        Length:         140
Percent Similarity:       65.62%       Matches:        19
Best Local Similarity:    59.38%       Conservative:    2
Query Match:              70.14%       Mismatches:      3
DB:                                    Indels:          8
                                       Gaps:            0

DELETED2 (1-81) x S78052 (1-140)

Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
        |||::::  |||     ||||||||||||||||||||||||||||
Db   56 GlyLys----GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 73

Qy   62 ACAACCCGTCTCTCAAGAGT 81
        |||||||||||||||
Db   73 yrAsnProSerLeuLysSer 79
```

RESULT 9
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl

A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <GRI>
A;Cross-references: GB:S33381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000231   Length: 140
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: Gaps: 0

DELETED2 (1-81) x A49045 (1-140)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
          ||::: ||| |||::: ||||||||||||
Db   61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||
Db   78 yrAsnProSerLeuLysSer 84

RESULT 10
B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: B23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000236   Length: 231
Score: 98.20   Matches: 19
Percent Similarity: 65.62%   Conservative: 2
Best Local Similarity: 59.38%   Mismatches: 3
Query Match: 70.14%   Indels: 8
DB: Gaps: 0

DELETED2 (1-81) x B23746 (1-231)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
          ||::: ||| |||::: ||||||||||||
Db   41 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 58

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||
Db   58 yrAsnProSerLeuLysSer 64

RESULT 11
PS0341
Ig heavy chain V-D-J region (RAMOS) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C;Accession: PS0341
R;Ratech, H.
Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell

---

A;Reference number: PS0341; MUID:92171937; PMID:1540170
A;Accession: PS0341
A;Molecule type: mRNA
A;Residues: 1-133 <RAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-38/Region: framework 1
F;39-43/Region: complementarity-determining 1
F;44-57/Region: framework 2
F;58-74/Region: complementarity-determining 2
F;75-106/Region: framework 3

Alignment Scores:
Pred. No.:   0.000245   Length: 133
Score: 98.00   Matches: 17
Percent Similarity: 94.74%   Conservative: 1
Best Local Similarity: 89.47%   Mismatches: 1
Query Match: 70.00%   Indels: 0
DB: Gaps: 0

DELETED2 (1-81) x PS0341 (1-133)

Qy   25 TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT 81
          ||||::: |||||||||||||||||||||||||||||||||
Db   55 TrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer 73

RESULT 12
G34964
Ig heavy chain V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
A;Molecule type: mRNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:   0.000763   Length: 97
Score: 94.20   Matches: 18
Percent Similarity: 62.50%   Conservative: 2
Best Local Similarity: 56.25%   Mismatches: 4
Query Match: 67.29%   Indels: 8
DB: Gaps: 0

DELETED2 (1-81) x G34964 (1-97)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACT 61
          ||::: || |||::: ||||||||||||
Db   42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlyGlyThrAsnT 59

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          |||||||||||||
Db   59 yrAsnProSerLeuLysSer 65

RESULT 13
S26905
Ig heavy chain V region (DP-70 / 4.19) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12419
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <SAN>
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	0.00148	Length:	98
Score:	92.00	Matches:	21
Percent Similarity:	48.89%	Conservative:	1
Best Local Similarity:	46.67%	Mismatches:	3
Query Match:	65.71%	Indels:	20
DB:	2	Gaps:	1

DELETED2 (1-81) x S26905 (1-98)

```
Qy      3 GGCGAGTCAGGATATTAGCAGC------------------------------------ 24
          ||| ||| ||||||||
Db     26 GlyGlySer----IleSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy 44

Qy     25 --------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCT 74
          ||:::  |||||| |||||||||||||||||||||||
Db     44 sGlyLeuGluTrpIleGlyIleIleHisSerGlySerThrAsnTyrAsnProSerLe 64

Qy     75 CAAGAGT 81
          |||||||
Db     64 uLysSer 66
```

RESULT 14
S78055
Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78055, S23720
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78055
A;Molecule type: mRNA
A;Residues: 1-145 <HAR>
A;Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkine
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23720
A;Molecule type: mRNA
A;Residues: 18-115 <HAW>
A;Cross-references: EMBL:X54445
A;Note: the authors translated the codon GCA for residue 67 as Arg
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F;18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	0.00151	Length:	145
Score:	92.00	Matches:	21
Percent Similarity:	48.89%	Conservative:	1
Best Local Similarity:	46.67%	Mismatches:	3
Query Match:	65.71%	Indels:	20
DB:	2	Gaps:	1

DELETED2 (1-81) x S78055 (1-145)

```
Qy      3 GGCGAGTCAGGATATTAGCAGC---
          ||| ||| ||||||||
Db     43 GlyGlySer----IleSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy 61

Qy     25 --------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCT 74
          ||:::  |||||| |||||||||||||||||||||||
Db     44 sGlyLeuGluTrpIleGlyIleIleHisSerGlySerThrAsnTyrAsnProSerLe 81

Qy     75 CAAGAGT 81
          |||||||
Db     81 uLysSer 83
```

RESULT 15
S14474
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S14474
R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H
submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Accession: S14474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <ESJ>
A;Cross-references: EMBL:X55591; NID:g37235; PIDN:CAA39929.1; PID:g1135354
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	0.00345	Length:	97
Score:	89.20	Matches:	18
Percent Similarity:	62.50%	Conservative:	2
Best Local Similarity:	56.25%	Mismatches:	4
Query Match:	63.71%	Indels:	8
DB:	2	Gaps:	0

DELETED2 (1-81) x S14474 (1-97)

```
Qy      2 GGGCGAGTCAGGATATTAGCAGC---
          ||:::  |||||| 
Db     42 GlyLys----GlyLeu----GluTrpIleGlyIleIleHisSerGlySerThrAsnT 59

Qy     62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||||||||
Db     59 yrAsnProSerLeuLysSer 65
```

Search completed: August 4, 2005, 20:05:40
Job time : 27 secs

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               GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     August  4, 2005, 19:40:06 ; Search time 116 Seconds
                                         (without alignments)
                                         715.145 Million cell updates/sec

Title:         DELETED2
Perfect score: 140
Sequence:      1 CGGGCGAGTCAGGATATTAG........ACAACCCGTCTCTCAAGAGT 81

Scoring table: BLOSUM62
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               Ygapop 10.0 , Ygapext  0.1
               Fgapop  6.0 , Fgapext  0.1
               Delop   6.0 , Delext   0.1

Searched:      1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:     3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3B/runat_04082005_120453_19612/app_query.fasta_1.263
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN_1_1_244 @runat_04082005_120453_19612 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :     UniProt_03:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	98.2	70.1	116	2	Q7Z3Y6	Q7z3y6 homo sapien
2	98.2	70.1	595	2	Q8WUX4	Q8wux4 homo sapien
3	98.2	70.1	597	2	Q6GMX5	Q6gmx5 homo sapien
4	98.2	70.1	597	2	Q9BU10	Q9bu10 homo sapien
5	98.2	70.1	625	2	Q96AA6	Q96aa6 homo sapien
6	92.2	65.9	597	2	Q9BQB8	Q9bqb8 homo sapien
7	92	65.7	576	2	Q6P4I8	Q6p4i8 homo sapien
8	87.2	62.3	146	1	HV2I_HUMAN	P06331 homo sapien
9	82.1	58.6	477	2	Q6GMX7	Q6gmx7 homo sapien
10	79.1	56.5	139	2	Q86SX2	Q86sx2 homo sapien
11	77.1	55.1	620	2	Q96EY0	Q96ey0 homo sapien
12	76.3	54.5	479	2	Q99M22	Q99m22 mus musculu
13	75.7	54.1	116	1	HV61_MOUSE	P18532 mus musculu
14	75.2	53.7	465	2	Q6GMX6	Q6gmx6 homo sapien
15	72.8	52.0	262	2	Q65ZI1	Q65zi1 mus musculu
16	71.3	50.9	116	1	HV60_MOUSE	P18531 mus musculu
17	71.2	50.9	119	2	Q9UL73	Q9UL73 homo sapien
18	71.2	50.9	476	2	Q6GMX1	Q6gmx1 homo sapien
19	69.1	49.4	478	2	Q6NYH3	Q6nyh3 homo sapien
20	68.6	49.0	150	2	O95973	O95973 homo sapien
21	68.2	48.7	478	2	Q7Z379	Q7z379 homo sapien
22	67.4	48.1	113	1	HV47_MOUSE	mus musculu
23	66.4	47.4	104	2	Q99CA9	human immun
24	66.4	47.4	106	2	Q6TJQ4	human immun
25	66.4	47.4	133	2	Q90QV6	human immun
26	65.9	47.1	496	2	Q96KX8	homo sapien
27	65.5	46.8	523	2	Q6QJ60	paraphlegop
28	65.5	46.8	523	2	Q6QJ62	paraphlegop
29	65.4	46.7	104	2	Q99CH3	human immun
30	65.4	46.7	130	2	Q9QL43	human immun
31	65.4	46.7	202	2	Q9IUP1	human immun
32	65.4	46.7	202	2	Q9IUR6	human immun
33	65.4	46.7	206	2	Q72N97	human immun
34	65.4	46.7	207	2	Q9IUQ5	human immun
35	65.4	46.7	212	2	Q9J783	human immun
36	65.4	46.7	220	2	Q9IUT6	human immun
37	65.4	46.7	231	2	Q9IQS9	human immun
38	65.4	46.7	489	2	Q80632	human immun
39	65.3	46.6	136	2	Q6LBQ5	mus musculu
40	65.3	46.6	137	1	HV46_MOUSE	mus musculu
41	64.4	46.0	130	2	Q7ZB82	human immun
42	64.4	46.0	131	2	Q90QT5	human immun
43	64.4	46.0	131	2	Q9QKY2	human immun
44	64.4	46.0	131	2	Q9QKY3	human immun
45	64.4	46.0	140	2	Q69BZ8	human immun

ALIGNMENTS

```
RESULT 1
Q7Z3Y6
ID   Q7Z3Y6       PRELIMINARY;      PRT;   116 AA.
AC   Q7Z3Y6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rearranged VH4-34 V gene segment (Fragment).
GN   Name=VH4-34;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564425; CAD92032.1; -.
DR   HSSP; P18532; 1KCV.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1
FT   NON_TER       116
SQ   SEQUENCE   116 AA;  12902 MW;  CE3D8A46616C908 CRC64;

Alignment Scores:
Pred. No.:                0.000436
Score:                    98.20
Percent Similarity:       65.62%        Length:         116
Best Local Similarity:    59.38%        Matches:         19
Query Match:              70.14%        Conservative:     2
DB:                       2             Mismatches:       3
                                        Indels:           8
                                        Gaps:             0

DELETED2 (1-81) x Q7Z3Y6 (1-116)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
```

```
Qy          42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
               |||::::     |||           |||||||||||||||||||||||
Db          62 ACAACCGTCTCTCAAGAGT 81
               |||||||||||||||||||
Qy          59 yrAsnProSerLeuLysSer 65


RESULT 2
Q8WUX4
ID   Q8WUX4          PRELIMINARY;       PRT;   595 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012235; AAH19235.2; -.
DR   PIR; G34964; G34964.
DR   HSSP; P01861; 1ADQ.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   595 AA;  65290 MW;  0D4B5077654571 4E CRC64;

Alignment Scores:
Pred. No.:              0.000538           Length:           595
Score:                  98.20              Matches:          19
Percent Similarity:     65.62%             Conservative:     2
Best Local Similarity:  59.38%             Mismatches:       3
Query Match:            70.14%             Indels:           8
DB:                                        Gaps:             0

DELETED2 (1-81) x Q8WUX4 (1-595)

Qy           2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
               |||::::     |||
Db          68 GlyLeu---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 85
```

```
Qy          62 ACAACCGTCTCTCAAGAGT 81
               |||||||||||||||||||
Db          85 yrAsnProSerLeuLysSer 91


RESULT 3
Q6GMX5
ID   Q6GMX5          PRELIMINARY;       PRT;   597 AA.
AC   Q6GMX5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073767; AAH73767.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65304 MW;  2A1E75F6AED85230 CRC64;

Alignment Scores:
Pred. No.:              0.000538           Length:           597
Score:                  98.20              Matches:          19
Percent Similarity:     65.62%             Conservative:     2
Best Local Similarity:  59.38%             Mismatches:       3
Query Match:            70.14%             Indels:           8
DB:                                        Gaps:             0

DELETED2 (1-81) x Q6GMX5 (1-597)

Qy           2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
```

```
Db       61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
            ||| :::   ||| :::    |||||||||||||||||||||||||||

Qy       62 ACAACCCGTCTCTCAAGAGT 81
            |||||||||||||||||||||
Db       78 yrAsnProSerLeuLysSer 84

RESULT 5
Q96AA6
ID   Q96AA6          PRELIMINARY;       PRT;     625 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strauberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.2; -.
DR   PIR; S15590; S15590.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE  625 AA;   68610 MW;  F62FAB3ADE7ECBFE CRC64;

Alignment Scores:
Pred. No.:                      0.000541        Length:              625
Score:                          98.20           Matches:             19
Percent Similarity:             65.62%          Conservative:        2
Best Local Similarity:          59.38%          Mismatches:          3
Query Match:                    70.14%          Indels:              8
DB:                             2               Gaps:                0

DELETED2 (1-81) x Q96AA6 (1-625)

Qy        2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
            ||| ::|                      ||||||||||||||||||||||||||||||||
Db        2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
```

```
Db       61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
            ||| :::   ||| :::    |||||||||||||||||||||||||||

Qy       62 ACAACCCGTCTCTCAAGAGT 81
            |||||||||||||||||||||
Db       78 yrAsnProSerLeuLysSer 84

RESULT 4
Q9BU10
ID   Q9BU10          PRELIMINARY;       PRT;     597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph.
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strauberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE  597 AA;   65274 MW;  2DAFA8FB7E055851 CRC64;

Alignment Scores:
Pred. No.:                      0.000538        Length:              597
Score:                          98.20           Matches:             19
Percent Similarity:             65.62%          Conservative:        2
Best Local Similarity:          59.38%          Mismatches:          3
Query Match:                    70.14%          Indels:              8
DB:                             2               Gaps:                0

DELETED2 (1-81) x Q9BU10 (1-597)

Qy        2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
            ||| ::|                      ||||||||||||||||||||||||||||||||
Db       61 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
```

RESULT 6

```
                      |||  .::.   ---    |||  |::.  |||||||||||||||
Qy    68  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT  85
              |||||||||||||  |||||||||||
Qy    62  ACAACCGTCTCTCAAGAGT  81
              |||||||||||||||||||
Db    85  yrAsnProSerLeuLysSer  91
```

```
Q9BQB8
ID   Q9BQB8           PRELIMINARY;     PRT;   597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE  597 AA;  65300 MW;  2DAFAD50A6375851 CRC64;
```

Alignment Scores:

```
Pred. No.:                  0.00355       Length:           597
Score:                      92.20         Matches:          18
Percent Similarity:         62.50%        Conservative:     2
Best Local Similarity:      56.25%        Mismatches:       4
Query Match:                65.86%        Indels:           8
DB:                         2             Gaps:             0
```

DELETED2 (1-81) x Q9BQB8 (1-597)

```
                      |||  .::   ---      |||  |::.  |||||||||||||||
Qy     2  GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT  61
              |||  .::      ---  |||  |::.  ||||||||||||||||||||||||
Db    61  GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlyIleThrAsnT  78
```

```
                      |||  .::.   ---    |||  |::.  |||||||||||||||
Qy    62  ACAACCGTCTCTCAAGAGT  81
              |||||||||||||
Db    78  yrAsnProSerLeuLysSer  84
```

RESULT 7

```
Q6P4I8
ID   Q6P4I8           PRELIMINARY;     PRT;   576 AA.
AC   Q6P4I8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHD protein.
GN   Name=IGHD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063384; AAH63384.1; -.
HSSP; P01820; 1A7N.
DR   InterPro; IPR003599; Ig-.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ   SEQUENCE  576 AA;  63363 MW;  FBB97C949D720F1E CRC64;
```

Alignment Scores:

```
Pred. No.:                  0.00377       Length:           576
Score:                      92.00         Matches:          21
Percent Similarity:         48.89%        Conservative:     1
Best Local Similarity:      46.67%        Mismatches:       3
Query Match:                65.71%        Indels:           20
DB:                         2             Gaps:             1
```

DELETED2 (1-81) x Q6P4I8 (1-576)

```
Qy    3 GGGCGAGTCAGGATATTAGCAGC------------------------------------ 24
          ||| |||| |||||||
Db   52 GlyGlySer----IleSerSerAsnTrpValArgGlnProProGlyLy             70

Qy   25 ------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCT       74
          ||| :::   ||||| ||||||||||||||||||||||||||||
Db   70 sGlyLeuTrpIleGlyLeuIleTyrHisSerGlySerThrAsnTyrAsnProSerLe    90

Qy   75 CAAGAGT 81
          |||||||
Db   90 uLysSer 92
```

RESULT 8
HV2I_HUMAN
```
ID   HV2I_HUMAN    STANDARD;      PRT;   146 AA.
AC   P06331;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205333; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT   repeat sequence in 5' flanking region.";
RL   Gene 33:181-189(1985).
DR   PIR; A02101; G1HUH2.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    146       Ig heavy chain V-II region ARH-77.
FT   DOMAIN       20    117       V segment.
FT   DOMAIN      118    127       D segment.
FT   DOMAIN      128    146       J segment.
FT   DISULFID     42    115       By similarity.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;   16228 MW;  8D7FD52BB218171F CRC64;
```

Alignment Scores:
```
Pred. No.:              0.0143
Score:                 87.20
Percent Similarity:    59.38%
Best Local Similarity: 56.25%
Query Match:           62.29%
DB:                     1
```

DELETED2 (1-81) x HV2I_HUMAN (1-146)

```
Qy    2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
          || |||||| ||||| ||||||    ||||||||||||||||||||||||||||||||
Db   62 GlyArg----GlyLeu---GluTrpIleGlyLeuIleAsnHisSerGlySerThrAsnT  79

Qy   62 ACAACCCGTCTCTCAAGAGT 81
          ||||||||||
Db   79 yrLysThrSerLeuLysSer 85
```

RESULT 9
Q6GMX7
```
ID   Q6GMX7          PRELIMINARY;       PRT;    477 AA.
AC   Q6GMX7;
```

```
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Guigo R.J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073765; AAH73765.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   477 AA;   51631 MW;  9FE59C09C50CFF85 CRC64;
```

Alignment Scores:
```
Pred. No.:              0.0828             Length:         477
Score:                 82.10              Matches:         19
Percent Similarity:    47.73%             Conservative:     2
Best Local Similarity: 43.18%             Mismatches:       4
Query Match:           58.64%             Indels:          19
DB:                     2                 Gaps:             1
```

DELETED2 (1-81) x Q6GMX7 (1-477)

```
Qy    3 GGGCGAGTCAGGATATTAGCAGC------------------------------------ 24
          ||| |||   |||||||
Db   45 GlyGlySer---IleSerSerTyrTyrTrpSerTrpIleArgGlnThrAlaGlyLysGl  63

Qy   25 ------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACCCGTCTCTCAA   77
          ||:::      ||||| ||||||||||||||||||||
Db   63 yLeuGluTrpIleGlyTyrIleSerHisSerGlySerThrTyrAsnProSerLeuLyJy  83

Qy   78 GAGT 81
          ||||
```

Db   83 sSer 84

RESULT 10
Q86SX2
ID   Q86SX2;   PRELIMINARY;   PRT;   139 AA.
AC   Q86SX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE   Homo sapiens (human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B cells;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248300; CAD62627.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
SQ   SEQUENCE   139 AA;   15573 MW;   7D1E2302410E4F8C CRC64;

Alignment Scores:
Pred. No.:   0.182
Score: 79.10
Percent Similarity: 47.73%
Best Local Similarity: 43.18%
Query Match: 56.50%
DB: 2

Length: 139
Matches: 19
Conservative: 2
Mismatches: 4
Indels: 19
Gaps: 1

DELETED2 (1-81) x Q86SX2 (1-139)

Qy   3 GGCGAGTCAGGATATTAGCAGC---------------------------- 24
      ||| ||| ||| ||||||||
Db   58 GlyGlySer----IleSerSerTyrTyrTrpSerTyrTyrTrpIleArgGlnProProGlyLysGl 76

Qy   25 ------TGGTTAGCCGAAATCAATCATAGTGAAGCACCAACTACACACCGTCTCCAA 77
      :::|||||||||||||||||||||||||||||||||||
Db   76 yLeuGluTrpIleGlyTyrIleTyrIleTyrSerGlySerThrAsnTyrAsnProSerLeuLy 96

Qy   78 GAGT 81
      ||||
Db   96 sSer 97

RESULT 11
Q96EY0
ID   Q96EY0;   PRELIMINARY;   PRT;   620 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

---

RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.2; -.
DR   PIR; S15590; S15590.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE   620 AA;   68125 MW;   990A1A4A6E8FF27B CRC64;

Alignment Scores:
Pred. No.:   0.413
Score: 77.10
Percent Similarity: 45.45%
Best Local Similarity: 43.18%
Query Match: 55.07%
DB: 2

Length: 620
Matches: 19
Conservative: 1
Mismatches: 5
Indels: 19
Gaps: 1

DELETED2 (1-81) x Q96EY0 (1-620)

Qy   3 GGCGAGTCAGGATATTAGCAGC---------------------------- 24
      ||| ||| ||| ||||||||
Db   52 GlyGlySer----IleSerSerTyrTyrTrpIleArgGlnProAlaGlyLysGl 70

Qy   25 ------TGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACTACACCGTCTCTCAA 77
      ||| :::|||||||||||||||||||||||||||||||
Db   70 yLeuGluTrpIleGlyArgIleTyrThrSerGlySerThrAsnTyrAsnProSerLeuLy 90

Qy   78 GAGT 81
      ||||
Db   90 sSer 91

RESULT 12
Q99M22
ID   Q99M22;   PRELIMINARY;   PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  51992 MW;  768E39A138918892 CRC64;

Alignment Scores:
Pred. No.:                  0.513         Length:        479
Score:                     76.30          Matches:        15
Percent Similarity:        37.04%         Conservative:    5
Best Local Similarity:     27.78%         Mismatches:      7
Query Match:               54.50%         Indels:         27
DB:                                       Gaps:            1

DELETED2 (1-81) x Q99M22 (1-479)

Qy      1 CGGGCGAGTCAGGATATTAGC----------------------------------------- 21
            ::: |||||||      ::||||
Db     31 LysProSerGlnSerLeuSerLeuThrCysSerValThrGlyTyrSerIleThrSerGly  50

Qy     22 -------------------------------------------AGCTGGTTAGCCGGAAATC 39
                                                       ||:::
Db     51 TyrTyrTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle  70

Qy     40 AATCAGTAGTGGAAGCACCAACTACAACCCGTCTCCAAGAGT 81
            ||::|||      |||::::||||:::
Db     71 AsnTyrAspGlySerAsnAsnTyrAsnProSerLeuLysAsn  84

RESULT 13
HV61_MOUSE
ID   HV61_MOUSE     STANDARD;      PRT;   116 AA.
AC   P18532;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region 1B43 precursor.
```

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OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during the
RT   primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
DR   PIR; JT0508; HVMS1B.
DR   PDB; 1KCS; X-ray; H=19-116.
DR   PDB; 1KCV; X-ray; H=19-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    116       Ig heavy chain V region 1B43.
FT   DOMAIN       19     48       Framework-1.
FT   DOMAIN       49     53       Complementarity-determining-1.
FT   DOMAIN       54     67       Framework-2.
FT   DOMAIN       68     84       Complementarity-determining-2.
FT   DOMAIN       85    116       Framework-3.
FT   DISULFID     40    114       By similarity.
FT   STRAND       21     25
FT   STRAND       29     30
FT   TURN         32     33
FT   TURN         36     43
FT   STRAND       47     49
FT   STRAND       52     58
FT   TURN         60     61
FT   TURN         64     71
FT   STRAND       72     73
FT   TURN         76     78
FT   STRAND       80     85
FT   TURN         86     91
FT   STRAND       92     95
FT   STRAND       96    101
FT   HELIX       106    108
FT   STRAND      110    116
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  13158 MW;  1CB54725368IFF74 CRC64;

Alignment Scores:
Pred. No.:                  0.517         Length:        116
Score:                     75.70          Matches:        16
Percent Similarity:        56.76%         Conservative:    5
Best Local Similarity:     43.24%         Mismatches:      3
Query Match:               54.07%         Indels:         13
DB:                                       Gaps:            1

DELETED2 (1-81) x HV61_MOUSE (1-116)

Qy      9 TCAGGATATTAGC------------------------------------------AGCTGGTTAGC 32
            ||||||||||| :::
Db     49 SerGlyTyr-SerTrpHisTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGl  68

Qy     33 CGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCCAAGAGT 81
            ||:::||||||||:::||||||||||||||||
Db     68 yTyrIleHisTyrSerGlyAsnThrSerTyrAsnProSerLeuLysSer  84

RESULT 14
Q6GMX6
ID   Q6GMX6         PRELIMINARY;   PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
```

DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Alignment Scores:
Pred. No.:
Score: 0.723   Length: 465
Percent Similarity: 75.20%   Matches: 16
Best Local Similarity: 56.25%   Conservative: 2
Query Match: 50.00%   Mismatches: 6
DB: 53.71%   Indels: 8
                           2   Gaps: 0

DELETED2 (1-81) x Q6GMX6 (1-465)

Qy   2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCAACT 61
         |||:::: ||| ||||::: |||||||||
Db   61 GlyLys---GlyLeu---GluTrpIleGlyArgIleTyrThrSerGlySerThrAsnT 78

Qy   62 ACAACCCGTCTCTCAAGAGT 81
         ||||||||||||||||||||
Db   78 yrAsnProSerLeuLysSer 84

RESULT 15
Q65ZI1
ID   Q65ZI1   PRELIMINARY;   PRT;   262 AA.
AC   Q65ZI1;

DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Anti-HIV-1 reverse transcriptase single-chain variable.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hybridoma;
RX   MEDLINE=96211469; PubMed=8648670;
RA   Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
RT   "Targeting human immunodeficiency virus type 1 reverse transcriptase
RT   by intracellular expression of single-chain variable fragments to
RT   inhibit early stages of the viral life cycle.";
RL   J. Virol. 70:3392-3400(1996).
DR   EMBL; U48716; AAB64342.1; -.
DR   GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   RNA-directed DNA polymerase.
SQ   SEQUENCE   262 AA; 27842 MW; 7DF20138E53865E4 CRC64;

Alignment Scores:
Pred. No.:   Length: 262
Score: 1.43   Matches: 16
Percent Similarity: 72.80   Conservative: 4
Best Local Similarity: 55.56%   Mismatches: 4
Query Match: 44.44%   Indels: 12
DB: 52.00%   Gaps: 1

DELETED2 (1-81) x Q65ZI1 (1-262)

Qy   9 TCAGGATATTAGCAGCTGGTTAGCCGAA------------------------------ 36
         ||||||| |||||||::: :::
Db 178 SerGlyTyr-TrpAsnTrpIleArgIleArgGlyAsnLysPheProGlyAsnLysLeuAspTyrMetGlyTy 197

Qy   37 -ATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT 81
         ||||||:::||||| ||| |||||||||||||||||||||||||
Db 197 rIleAsnTyrSerGlyAspThrTyrTyrAsnProSerLeuLysSer 212

Search completed: August 4, 2005, 20:04:46
Job time : 120 secs